TTGAAGGCAG CCAGATCTGT TAAACTCTGT CCTTTCCCTC TCCGGAAGAG CAGCATGAAG
CTGGCATTCC TCTTCCTTGG CCCCATGGCC CTCCTCCTTC TGGCTGGCTA TGGCTGTGTC
CTCGGTGCCT CCAGTGGGAA CCTGCGCACC TTTGTGGGCT GTGCCGTGAG GGAGTTTACT
TTCCTGGCCA AGAAGCCAGG CTGCAGGGGC CTTCGGATCA CCACGGATGC CTGCTGGGGT
CGCTGTGAGA CCTGGGAGAA ACCCATTCTG GAACCCCCCT ATATTGAAGC CCATCATCGA
GTCTGTACCT ACAACGAGAC CAAACAGGTG ACTGTCAAGC TGCCCAACTG TGCCCCGGGA
GTCGACCCCT TCTACACCTA TCCCGTGGCC ATCCGCTGTG ACTGCGGAGC CTGCTCCACT
GCCACCACGG AGTGTGAGAC CATCTGA (SEQ ID NO: 1)

ATGAACAAGA AGAGGGTGAT GTTCCCTGTC CTGCAGCTTC TGGTTTTAGC CCTGTGTCTC
AGCACCGCTG CAGGATCCAA TATAAGTCTG AGAACGTTCA TTGGATGTGC TGTGAGGGAA
TTCACATTCT TAGCAAAGAA ACCTGGCTGC AGAGGTCTGC GTGTGACTAC TGATGCCTGC
TGGGGGCGCT GTGAGACCTG TGAGAAGCCA TCCCTAGATC CTCCGTACAT AGAAGCCCAC
CACAGAGTCT GCACTTACAA TGAAACTAAA CTGGTTACTG TAATACTGCC AAACTGCAGC
CCAGACATTG ACCCATTCTT TACCTACCCA GTTGCCATTA GATGTGACTG TGACATGTGG
TCCACTTCTA CTACAGAATG T (SEQ ID NO: 3)

TRADOCS:1357679.1(T3LB01!.DOC)

Fig. 1

MKLAFLLLGP MALLLLAGYG CLGASSGNLR TFVGCAVREF TFLAKKPGCR
GLRITTDACW GRCETWEKPI LEPPYIEAHH RVCTYNETKQ VTVKLPNCAP
GVDPFYTYPV AIRCDCGACS TATTECETI (SEQ ID NO: 2)

MNKKRVKFPV LQLLVLALCL STAAGSNISL RTFIGCAVRE FTFLAKKPGC
RGLRVTTDAC WGRCETCEKP SLDPPYIEAH HRVCTYNETK LVTVILLPNC
SPDIDPFFTY PVAIRCDCMW STSTTEC (SEQ ID NO: 4)

TRADOCS:1357827.1(T3PF01!.DOC)

Fig.2

MKLAFLLLGPMALLLLAGYGCLG (SEQ ID NO: 10)

TRADOCS:1357861.1(T3QD01!.DOC)

Fig. 3

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ttgaaggcag ccagatctgt taaactctgt cctttccctc tccggaagag cagc**atgaag**
M K
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L A F L L L G P M A L L L L A G Y G C
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F L A K K P G C R G L R I T T D A C W G
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R C E T W E < intron ----------
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Fig. 4A

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end of intron > K P I L
aaccccccta tattgaagcc catcatcgag tctgtaccta caacgagacc aaacaggtga
E P P Y I E A H H R V C T Y N E T K Q V
ctgtcaagct gcccaactgt gccccgggag tcgacccctt ctacacctat cccgtggcca
T V K L P N C A P G V D P F Y T Y P V A
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Fig. 4B

```
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aaaacagaaa taaaatatgt aactaatagc tatctcattt agccttaaaa acttattaaa
        ^ poly(A) ?
ctaaactcat gttttagagt atgatgttct cccaaagcta tggcaaaatg gccaatcaca
agtattcttc cccatttatc atattttcaa tttaagttgt aacttactaa actcagaaat
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gttccttttt cataatgtgc caagaaaacc tatattaatg ccaataaagc atgtcctctg
                                              ^ poly(A) ?
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(SEQ ID NO:78)
TRADOCS:1357757.1(T3NH01!.DOC)
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Fig. 4C

```
hLHbeta         ------MEMLQGLLLLLLLSMGGAWASREPLRPWCHPINAILAVEKEGCPVCITVNTTIC
hCGbeta         ------MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTIC
hFSHbeta        ---------MKTLQFFFLFCCWKAICCN-S----CELTNITIAIEKEECRFCISINTTWC
hTSHbeta        ------MTALFLMSMLFGLACGQAMSF-------CIPTEYTMHIERRECAYCLTINTTIC
beta5           MKLAFLLLGPMALLLLAGYGCLGASSGNLRTFVGCAVREFTFLAKKPGCR-GLRITTDAC
                            : ::       : .        *   :  :  ::  *   : :.*  *

hLHbeta         AGYCPTMMRVLQAVLPPLP--QVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGP
hCGbeta         AGYCPTMTRVLQGVLPALP--QVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCAL
hFSHbeta        AGYCYTRDLVYKD--PARPKIQKTCTFKELVYETVRVPGCAHHADSLYTYPVATQCHCGK
hTSHbeta        AGYCMTRDINGKLFLPKYALSQDVCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGK
beta5           WGRCETWEKPILEP-PYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGA
                 * * *         *     : .*.:.:    ::.:*.*.  . .  ::.**  * *.

hLHbeta         CRRSTSDCGGPKDHPLTCDHP-------------------QLSG-----LLFL (SEQ ID NO: 6)
hCGbeta         CRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ (SEQ ID NO: 8)
hFSHbeta        CDSDSTDCTVRGLGPSYCSFG-------------------EMKE--------- (SEQ ID NO: 7)
hTSHbeta        CNTDYSDCIHEAIKTNYCTKP-------------------QKSYLVGFSV--- (SEQ ID NO: 9)
beta5           CSTATTECETI------------------------------------------ (SEQ ID NO: 2)
                *    ::*
```

TRADOCS:1357838.1(T3PQ01!.DOC)

Fig. 5

	beta5	**hFSH**	**hCG**	**hLH**	**hTSH**
beta5	--	36 %	31 %	35 %	34 %
hFSH	50 %	--	40 %	41 %	40 %
hCG	48 %	60 %	--	86 %	47 %
hLH	56 %	60 %	90 %	--	41 %
hTSH	50 %	58 %	59 %	53 %	--

Fig. 6

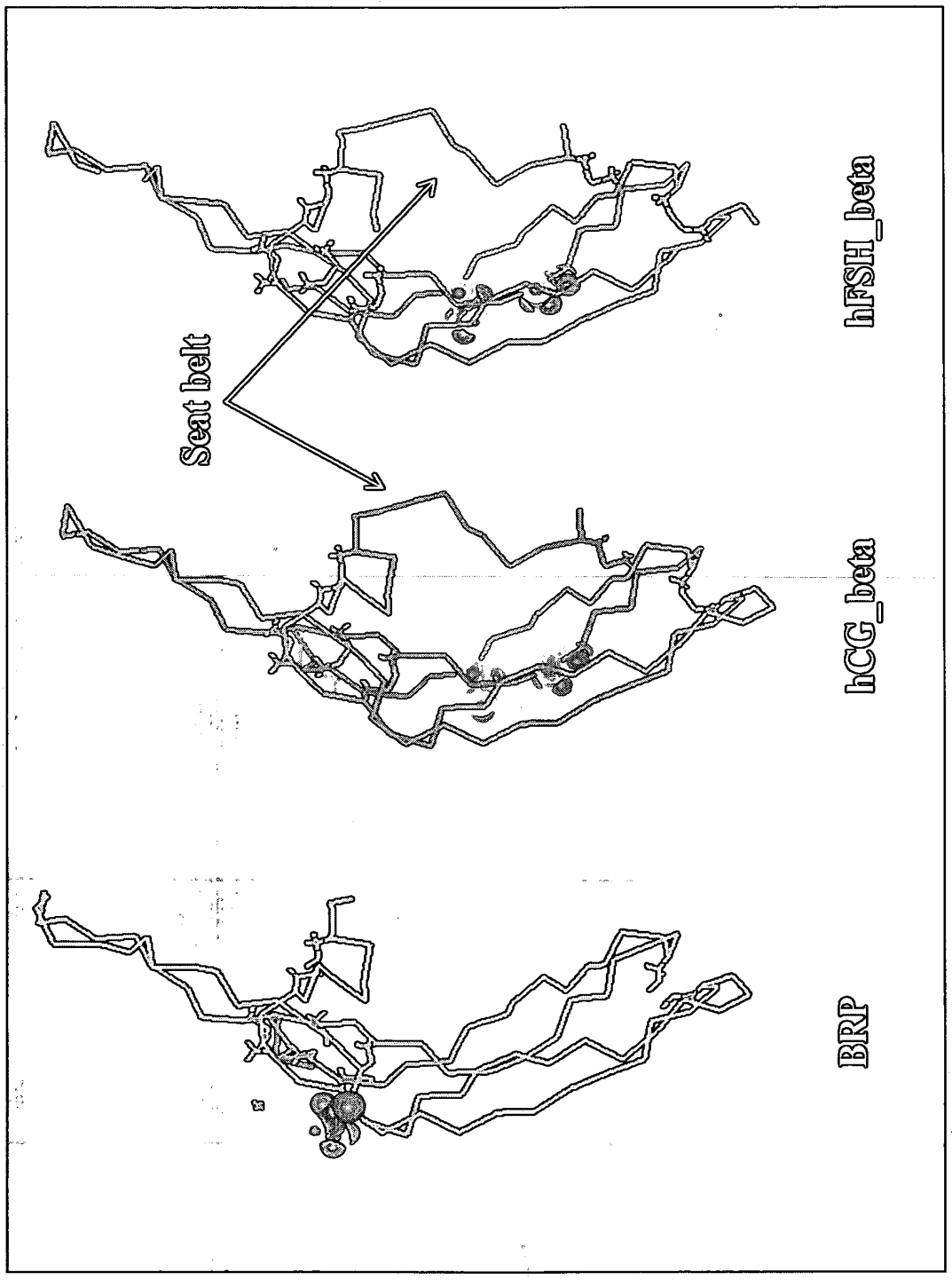


Fig. 7A

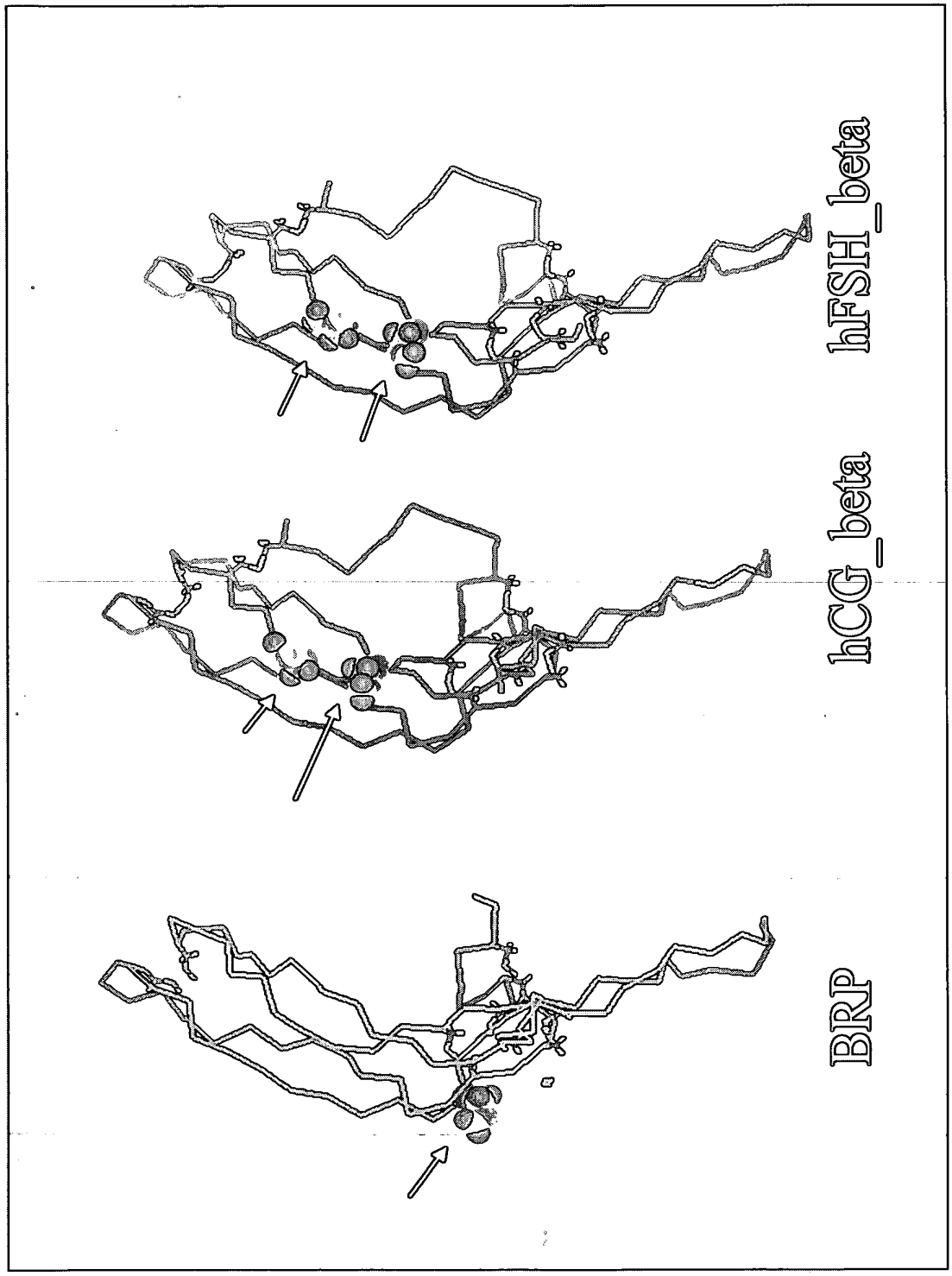


Fig. 7B

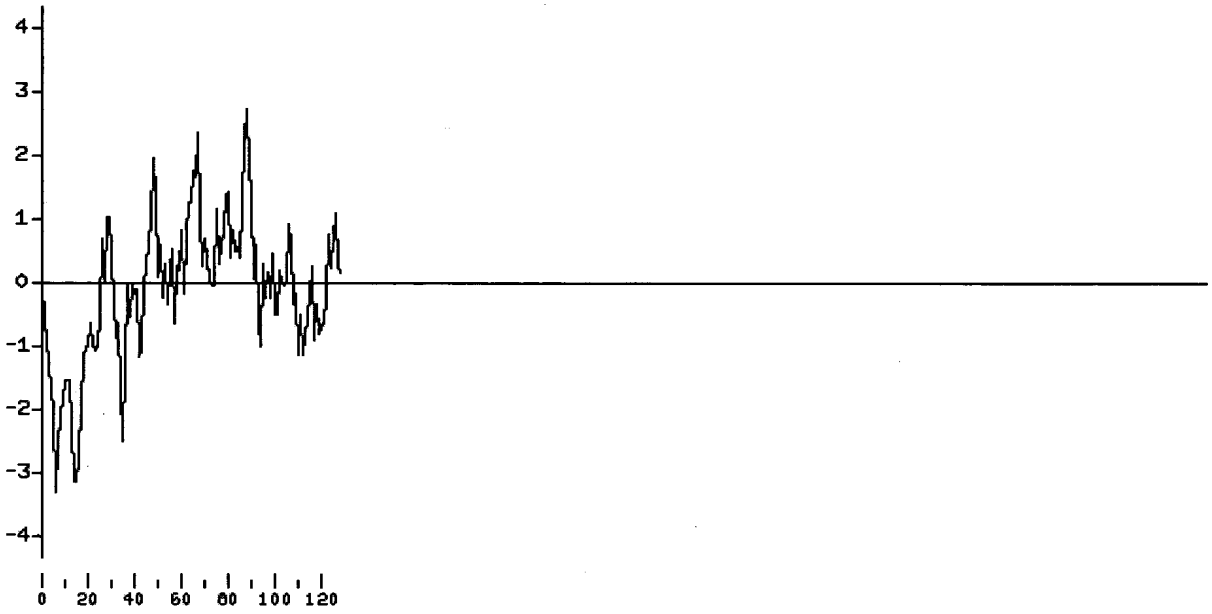


Fig. 8

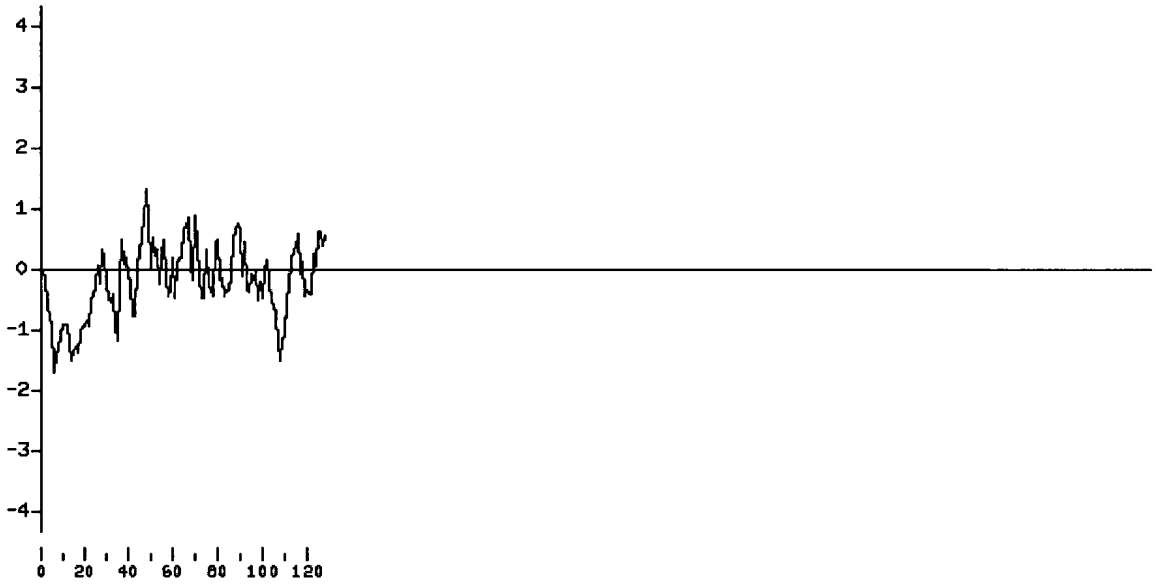


Fig. 9

MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYC
ETWEKPILEPPYIEAHHRV**CNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRR**
STTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ (SEQ ID NO:13)

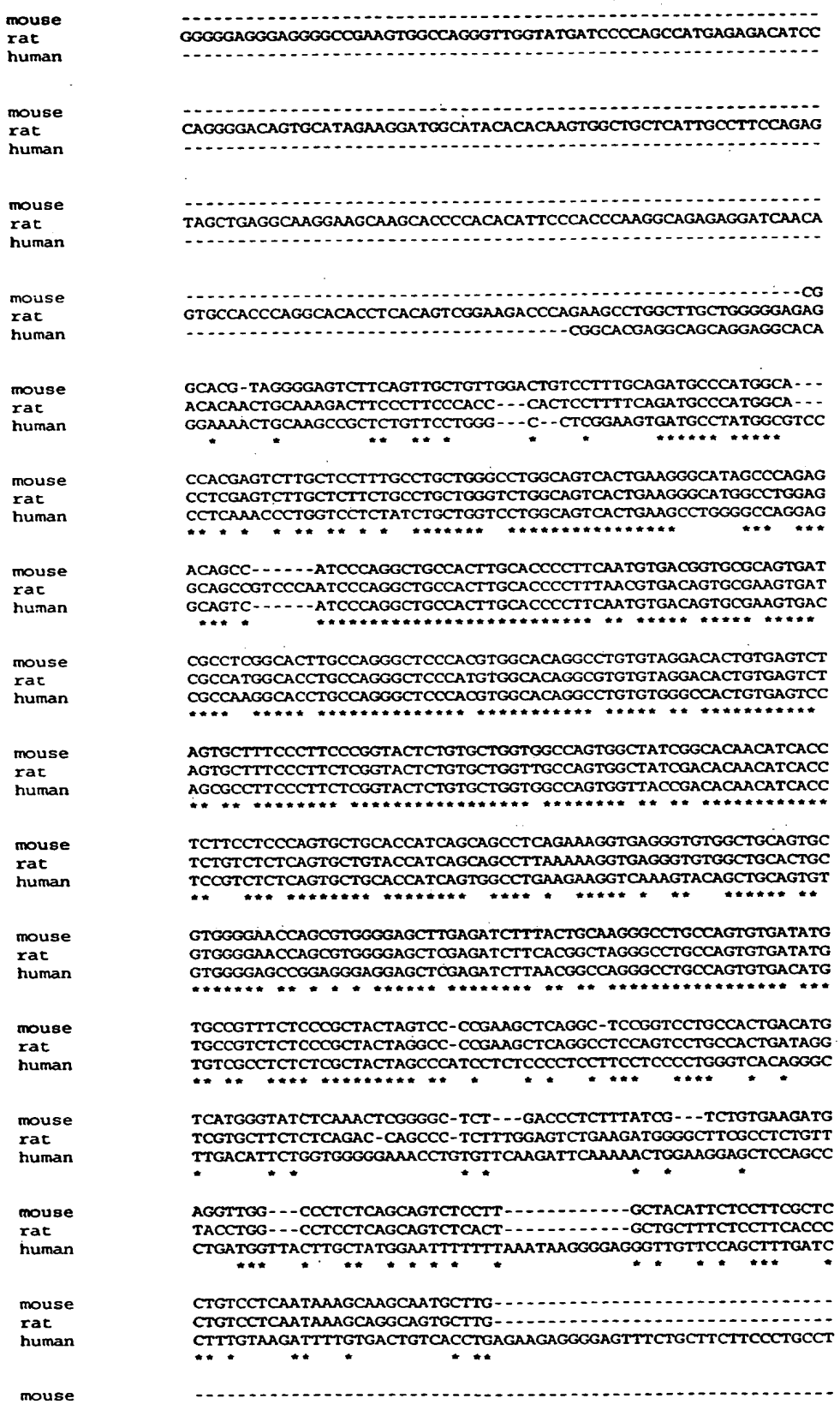
TRADOCS:1362466.1(T7@@01!.DOC)

Fig. 10

MKLAFLLLGPMALLLLAGYGCLGASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTDA
CWGRCETWEKPILEPPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDC
GACSTATTEC**TVRGLGPSYCSFGEMKE** (SEQ ID NO: 14)

TRADOCS:1362458.1(T7@201!.DOC)

Fig. 11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rat
human
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CGGCACGAGGCAGCAGGAGGCACA
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GGAAAACTGCAAGCCGCTCTGTTCCTGGG---C--CTCGGAAGTGATGCCTATGGCGTCC
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GCAGTC------ATCCCAGGCTGCCACTTGCACCCCTTCAATGTGACAGTGCGAAGTGAC
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CTGTCCTCAATAAAGCAGGCAGTGCTTG----------
CTTTGTAAGATTTTGTGACTGTCACCTGAGAAGAGGGGAGTTTCTGCTTCTTCCCTGCCT
mouse

Fig. 12A

```
rat       ------------------------------------------------------------
human     CTGCCTGGCCCTTCTAAACCAATCTTTCATCATTTTACTTCCCTCTTTGCCCTTACCCCT

mouse     ----------------------  (SEQ ID NO:19)
rat       ----------------------  (SEQ ID NO:21)
human     AAATAAAGCAAGCAGTTCTTG   (SEQ ID NO:17)
```

Fig. 12B

```
mouse     MPMA-PRVLLLCLLGLAVTEGHSPETA--IPGCHLHPFNVTVRSDRLGTCQGSHVAQACV
rat       MPMA-PRVLLFCLLGLAVTEGHGLEAAVPIPGCHLHPFNVTVRSDRHGTCQGSHVAQACV
human     MPMASPQTLVLYLLVLAVTEAWGQEAV--IPGCHLHPFNVTVRSDRQGTCQGSHVAQACV
          **** *:.*:: ** *****. . *:.  ********************* ************
                                      ^

mouse     GHCESSAFPSRYSVLVASGYRHNITSSSQCCTISSLRKVRVWLQCVGNQRGELEIFTARA
rat       GHCESSAFPSRYSVLVASGYRHNITSVSQCCTISSLKKVRVWLHCVGNQRGELEIFTARA
human     GHCESSAFPSRYSVLVASGYRHNITSVSQCCTISGLKKVKVQLQCVGSRREELEILTARA
          ************************** *******.*:**:* *:***.:* ****:****

mouse     CQCDMCRFSRY Seq. ID No: 20
rat       CQCDMCRLSRY Seq. ID No: 22
human     CQCDMCRLSRY Seq. ID No: 18
          *******.***
```

Fig. 13

```
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..51 ACACACAGGTCCTTTCCAGAGACAGCTGCTCACACTCACACCCATACACA
.101 CACACACACACACACAAAGGCAGATACAGGGAAAAGGCAGCACCATTCAG
.151 GCACACCTCACCTGTCAGACCAGCCAGCCCTGGCTCACTCACCTGGAATG
.201 CAGTATTTAAAGAACTCGCCATCCCACCTGCACACCCACGTAGAGACATC
.251 TCCCCACTGTGTTTCAGATGCCTATGGCGTCCCCTCAAACCCTGGTCCTC
.301 TATCTGCTGGTCCTGGCAGTCACTGAAGCCTGGGGCCAGGAGGCAGTCAT
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.601 GGCTCCCACGTGGCACAGGCCTGTGTGGGCCACTGTGAGTCCAGCGCCTT
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.701 CCTCCGTCTCTCAGTGCTGCACCATCAGTGGCCTGAAGAAGGTGAGGAGG
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.851 CCCGCAGGTCAAAGTACAGCTGCAGTGTGTGGGGAGCCGGAGGGAGGAGC
.901 TCGAGATCTTCACGGCCAGGGCCTGCCAGTGTGACATGTGTCGCCTCTCT
.951 CGCTACTAGCCCATCCTCTCCCCTCCTTCCTCCCCTGGGTCACAGGGCTT
1001 GACATTCTGGTGGGGGAAACCTGTGTTCAAGATTCAAAAACTGGAAGGAG
1051 CTCCAGCCCTGATGGTTACTTGCTATGGAATTTTTTTAAATAAGGGGAGG
1101 GTTGTTCCAGCTTTGATCCTTTGTAAGATTTTGTGACTGTCACCTGAGAA
1151 GAGGGGAGTTTCTGCTTCTTCCCTGCCTCTGCCTGGCCCTTCTAAACCAA
1201 TCTTTCATCATTTTACTTCCCTCT(SEQ ID NO:23)
```

Fig. 14

```
hFSHa   MDYYRKYAAIFLVTLSVFLHVLHSAPDVQDCPECTLQENPFFS-------QPG
hARP       MPMASPQTLVLYLLVLAVTEAWGQEAVIPGCHLHPFNVTVRSDRQGTCQG
hFSHb        MKTLQFFFLFCCWKAICC--------NSCELTNITIAIEKEECRFCIS

hFSHa       APILQ-CMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVM
hARP        SHVAQACVGHCESSAFPSRYSVLVASGYRHNITSVSQCCTISGLKKVKVQ
hFSHb       INTTW-CAGYCYTRDLVYKD---------PARPKIQKTCTFKELVYETVR

hFSHa       ---------GGFKVENHTACHCSTCYYHKS (SEQ ID NO: 10)
hARP        -LQCVGSRREELEIFTARACQCDMCRLSRY (SEQ ID NO: 2)
hFSHb       VPGCAHHADSLYTYPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEMKE
                                                (SEQ ID NO: 11)
```

Fig. 15

```
DNA: AGATGGCGAAGAAAATTCCAGGGAAGGGAGAATCACTGCACAGAGGGCTGA
DNA: CACACAGGTCCTTTCCAGAGACAGCTGCTCACACTCACACCCATACACACA
DNA: CACACACACACACAAAGGCAGATACAGGGAAAAGGCAGCACCATTCAGGCA
DNA: CACCTCACCTGTCAGACCAGCCAGCCCTGGCTCACTCACCTGGAATGCAGT
DNA: ATTTAAAGAACTCGCCATCCCACCTGCACACCCACGTAGAGACATCTCCCC
DNA: ACTGTGTTTCAGATGCCTATGGCGTCCCCTCAAACCCTGGTCCTCTATCTG
 +1:              M  P  M  A  S  P  Q  T  L  V  L  Y  L

DNA: CTGGTCCTGGCAGTCACTGAAGCCTGGGGCCAGGAGGCAGTCATCCCAGGC
 +1: L  V  L  A  V  T  E  A  W  G  Q  E  A  V  I  P  G

DNA: TGCCACTTGCACCGTGAGTACCTCTGGGACCGGAGGGCTAGGAGCAGTGGA
 +1: C  H  L  H  P

DNA: GGTTCTGGGTGGGAGCAAAGAGCTGACAGAGTGGACGGTGGGGCAGGCAGC
DNA: ACCCTAAAGGGCCCCACACTGAGGCACAGGCAACGGGAGCTGGGGCGAGGC
DNA: AAACCTTGGCAGAGGCGCCGTCTACTGCTTGCCTATCTCCTTCTAGCCTTC
 +1:                                                   F

DNA: AATGTGACAGTGCGAAGTGACCGCCAAGGCACCTGCCAGGGCTCCCACGTG
 +1: N  V  T  V  R  S  D  R  Q  G  T  C  Q  G  S  H  V

DNA: GCACAGGCCTGTGTGGGCCACTGTGAGTCCAGCGCCTTCCCTTCTCGGTAC
 +1: A  Q  A  C  V  G  H  C  E  S  S  A  F  P  S  R  Y

DNA: TCTGTGCTGGTGGCCAGTGGTTACCGACACAACATCACCTCCGTCTCTCAG
 +1: S  V  L  V  A  S  G  Y  R  H  N  I  T  S  V  S  Q

DNA: TGCTGCACCATCAGTGGCCTGAAGAAGGTGAGGAGGGCCCGGGCCCGGTGG
 +1: C  C  T  I  S  G  L  K  K

DNA: ATGGACGCTGGGGTCGCGGGAAGACCAGAGAGATGGAGATCCTAGACAGCC
DNA: CTGAGAAAGGGGACTGCAGCACGGACTCCCCTCTCCCGCAGGTCAAAGTAC
 +3:                                                   V  K  V  Q

DNA: AGCTGCAGTGTGTGGGGAGCCGGAGGGAGGAGCTCGAGATCTTCACGGCCA
 +3:    L  Q  C  V  G  S  R  R  E  E  L  E  I  F  T  A  R

DNA: GGGCCTGCCAGTGTGACATGTGTCGCCTCTCTCGCTACTAGCCCATCCTCT
 +3:    A  C  Q  C  D  M  C  R  L  S  R  Y  *

DNA: CCCCTCCTTCCTCCCCTGGGTCACAGGGCTTGACATTCTGGTGGGGGAAAC
DNA: CTGTGTTCAAGATTCAAAAACTGGAAGGAGCTCCAGCCCTGATGGTTACTT
DNA: GCTATGGAATTTTTTTTAAATAAGGGGAGGGTTGTTCCAGCTTTGATCCTTT
DNA: GTAAGATTTTGTGACTGTCACCTGAGAAGAGGGGAGTTTCTGCTTCTTCCC
DNA: TGCCTCTGCCTGGCCCTTCTAAACCAATCTTTCATCATTTTACTTCCCTCT
                                                    (SEQ ID NO: 79)
```

Fig. 16

Northern Blot of ARP - human cDNA probe and blot
(C. He – 3/24/00: 4 day exposure)

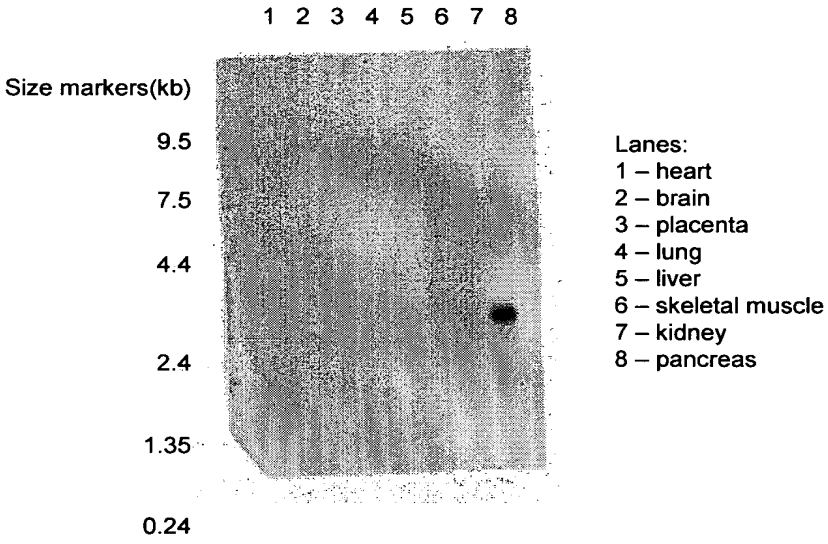


Fig. 17

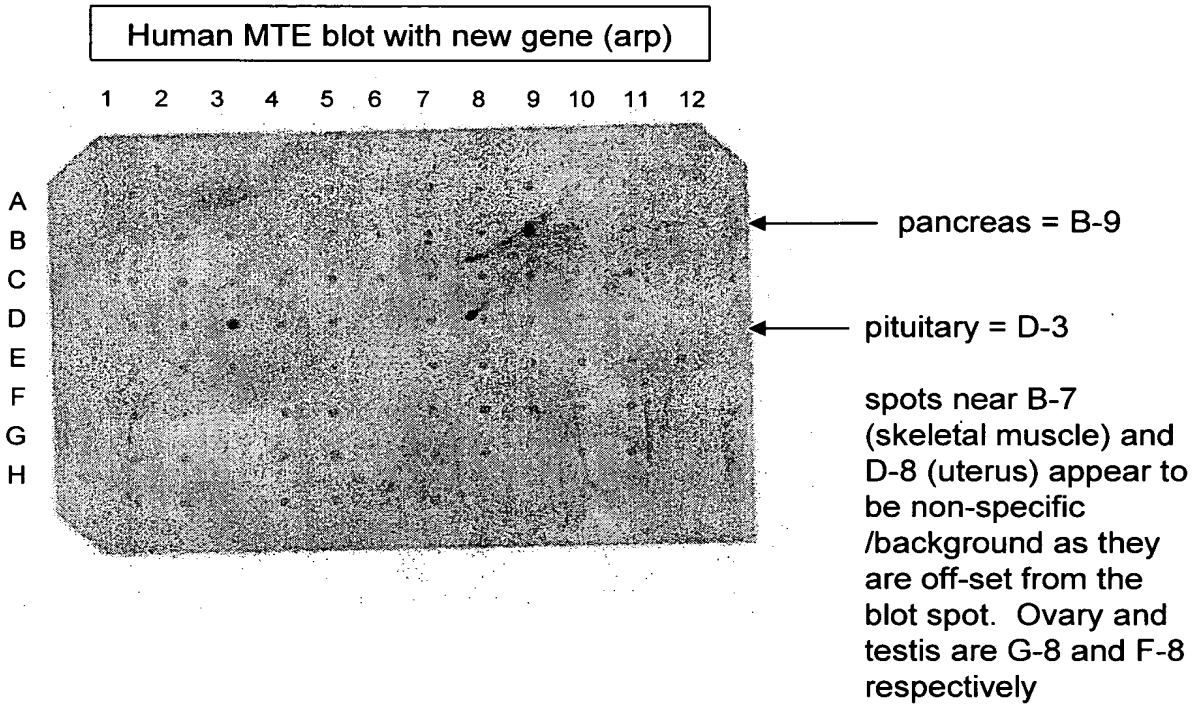

Human MTE blot with new gene (arp)
1 2 3 4 5 6 7 8 9 10 11 12
A
B
C
D
E
F
G
H
pancreas = B-9
pituitary = D-3
spots near B-7 (skeletal muscle) and D-8 (uterus) appear to be non-specific /background as they are off-set from the blot spot. Ovary and testis are G-8 and F-8 respectively

Fig. 18

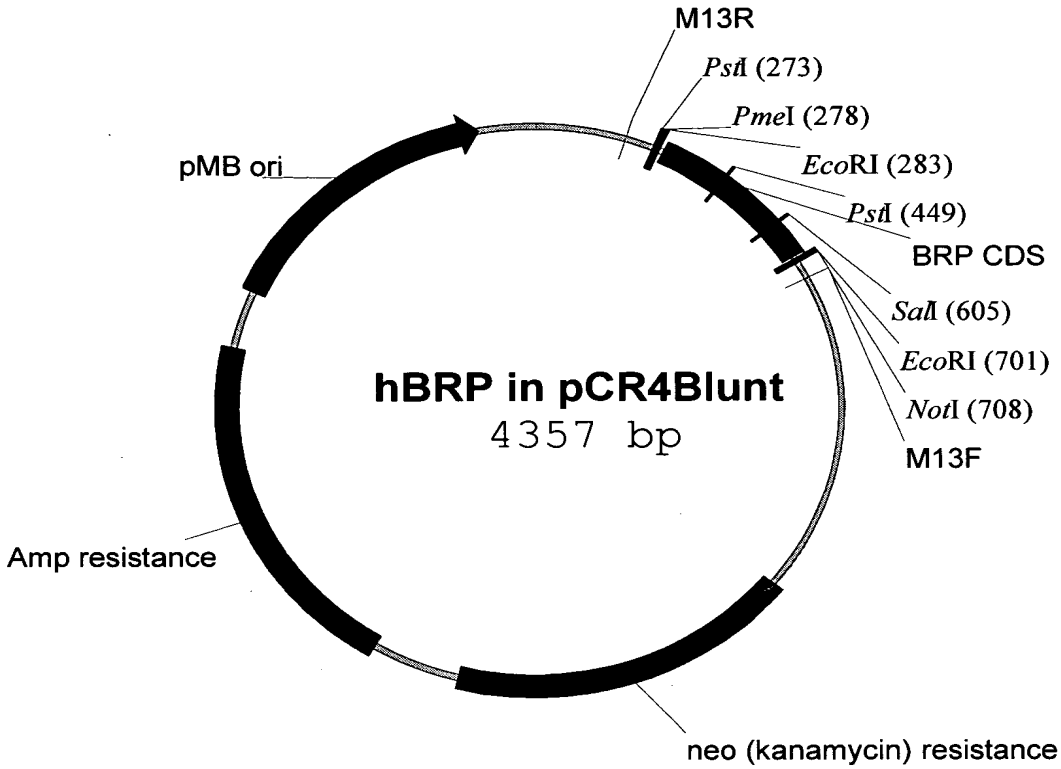


Fig. 19A

```
      EcoRI
      ~~~~~~
                          M  K  L  A  F     L  F  L     G  P  M     A  L  L  L     L  A  G  ·
281   CGAATTCGCC CTTCAGCATG AAGCTGGCAT TCCTCTTCCT TGGCCCCATG GCCCTCCTCC TTCTGGCTGG

      .  Y  G  C     V  L  G  A     S  S  G     N  L  R     T  F  V  G     C  A  V     R  E  F
351   CTATGGCTGT GTCCTCGGTG CCTCCAGTGG GAACCTGCGC ACCTTTGTGG GCTGTGCCGT GAGGGAGTTT
                                PstI
                               ~~~~~~~
      T  F  L  A     K  K  P     G  C  R     G  L  R  I     T  T  D     A  C  W     G  R  C  E  ·
421   ACTTTCCTGG CCAAGAAGCC AGGCTGCAGG GGCCTTCGGA TCACCACGGA TGCCTGCTGG GGTCGCTGTG

      .. T  W  E     K  P  I     L  E  P  P     Y  I  E     A  H  H     R  V  C  T     Y  N  E  ·
491   AGACCTGGGA GAAACCCATT CTGGAACCCC CCTATATTGA AGCCCATCAT CGAGTCTGTA CCTACAACGA
                                                    SalI
                                                   ~~~~~~~
      .  T  K  Q     V  T  V  K     L  P  N     C  A  P     G  V  D  P     F  Y  T     Y  P  V
561   GACCAAAACAG GTGACTGTCA AGCTGCCCAA CTGTGCCCCG GGAGTCGACC CCTTCTACAC CTATCCCGTG
                                                                                    EcoRI
      A  I  R  C     D  C  G     A  C  S     T  A  T  T     E  C  E     T  I  * (SEQ ID NO:81)
631   GCCATCCGCT GTGACTGCGG AGCCTGCTCC ACTGCCACCA CGGAGTGTGA GACCATCTGA GGCAAGGGCG (SEQ ID NO: 82)
```

Fig. 19B

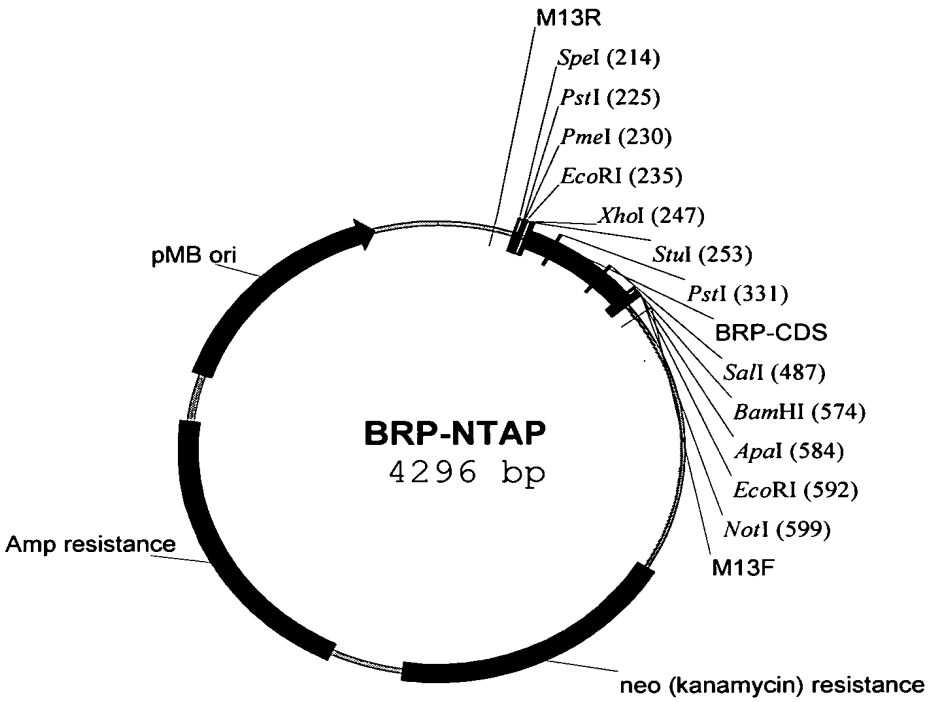


Fig. 20A

```
                        PmeI
                      ~~~~~~~~~~
                PstI           EcoRI          XhoI
               ~~~~~~~         ~~~~~~~       ~~~~~~~
                                                    A  S  S   G  N  L  R   T  F  V ·
 211   GGACTAGTCC TGCAGGTTTA AACGAATTCG CCCTTCTCGA GGCCTCCAGT GGGAACCTGC GCACCTTTGT
                                                      PstI
                                                     ~~~~~~~
       .  G  C  A   V  R  E  F   T  F  L   A  K  K   P  G  C  R   G  L  R   I  T  T
 281   GGGCTGTGCC GTGAGGGAGT TTACTTTCCT GGCCAAGAAG CCAGGCTGCA GGGGCCTTCG GATCACCACG

        D  A  C  W   G  R  C   E  T  W   E  K  P  I   L  E  P   P  Y  I   E  A  H  H ·
 351   GATGCCTGCT GGGGTCGCTG TGAGACCTGG GAGAAACCCA TTCTGGAACC CCCCTATATT GAAGCCCATC
                                                                          SalI
       .. R  V  C   T  Y  N   E  T  K  Q   V  T  V   K  L  P   N  C  A  P   G  V  D ·
 421   ATCGAGTCTG TACCTACAAC GAGACCAAAC AGGTGACTGT CAAGCTGCCC AACTGTGCCC CGGGAGTCGA
       .
       ~
       .  P  F  Y   T  Y  P  V   A  I  R   C  D  C   G  A  C  S   T  A  T   T  E  C
 491   CCCCTTCTAC ACCTATCCCG TGGCCATCCG CTGTGACTGC GGAGCCTGCT CCACTGCCAC CACGGAGTGT
                          ApaI                  NotI
                         ~~~~~~~               ~~~~~~~~~
                    BamHI                EcoRI
                    ~~~~~~              ~~~~~~
        E  T  I  * (SEQ ID NO: 83)
 561   GAGACCATCT GAGGATCCGG GCCCAAGGGC GAATTCGCGG CCGCTAAATT CAATTCGCCC TATAGTGAGT
(SEQ ID NO:84)
```

Fig. 20B

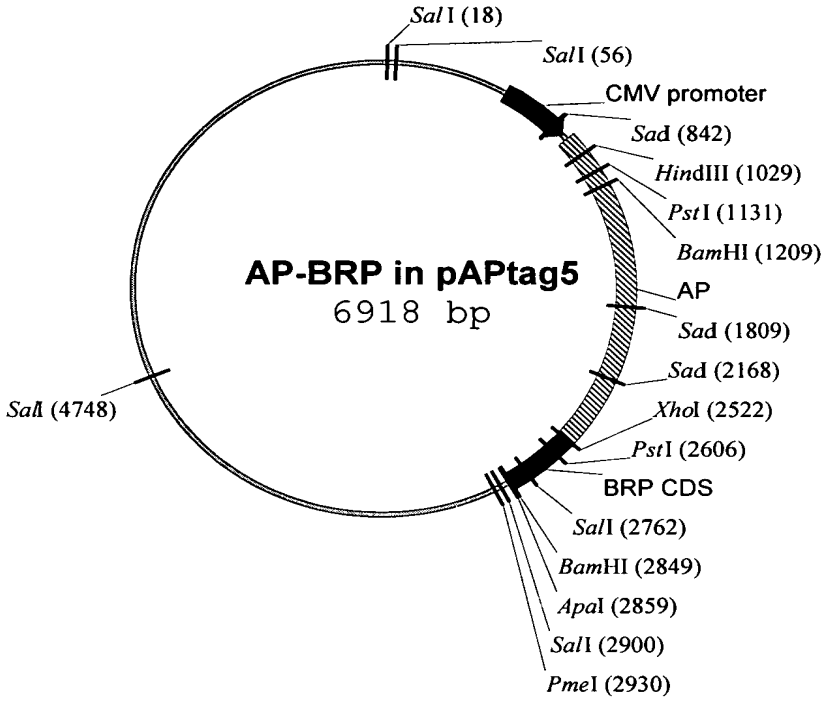


Fig. 21A

Alkaline phosphatase

```
      . L  E  P  Y  T  A  C  D  L  A  P  P  A  G  T  T  D  A  A  H  P  G  Y
2451  CCTGGAGCCC TACACCGCCT GCGACCTGGC GCCCCCCGCC GGCACCACCG ACGCCGCGCA CCCGGGTTAT
       XhoI
      ~~~~~~  BRP
       L  E  A  S  S  G  N  L  R  T  F  V  G  C  A  V  R  E  F  T  F  L  A  K ·
2521  CTCGAGGCCT CCAGTGGGAA CCTGCGCACC TTTGTGGGCT GTGCCGTGAG GGAGTTTACT TTCCTGGCCA
                PstI
               ~~~~~~
      .. K  P  G  C  R  G  L  R  I  T  T  D  A  C  W  G  R  C  E  T  W  E  K ·
2591  AGAAGCCAGG CTGCAGGGGC CTTCGGATCA CCACGGATGC CTGCTGGGGT CGCTGTGAGA CCTGGGAGAA

      . P  I  L  E  P  P  Y  I  E  A  H  H  R  V  C  T  Y  N  E  T  K  Q  V
2661  ACCCATTCTG GAACCCCCCT ATATTGAAGC CCATCATCGA GTCTGTACCT ACAACGAGAC CAAACAGGTG
                                      SalI
                                     ~~~~~~
       T  V  K  L  P  N  C  A  P  G  V  D  P  F  Y  T  Y  P  V  A  I  R  C  D ·
2731  ACTGTCAAGC TGCCCAACTG TGCCCCGGGA GTCGACCCCT TCTACACCTA TCCCGTGGCC ATCCGCTGTG
                                                          ApaI
                                                         ~~~~~~~
                                                   BamHI
                                                  ~~~~~~
      .. C  G  A  C  S  T  A  T  T  E  C  E  T  I  * (SEQ ID NO:85)
2801  ACTGCGGAGC CTGCTCCACT GCCACCACGG AGTGTGAGAC CATCTGAGGA TCCGGGCCCG AACAAAAACT
(SEQ ID NO:86)
```

Fig. 21B

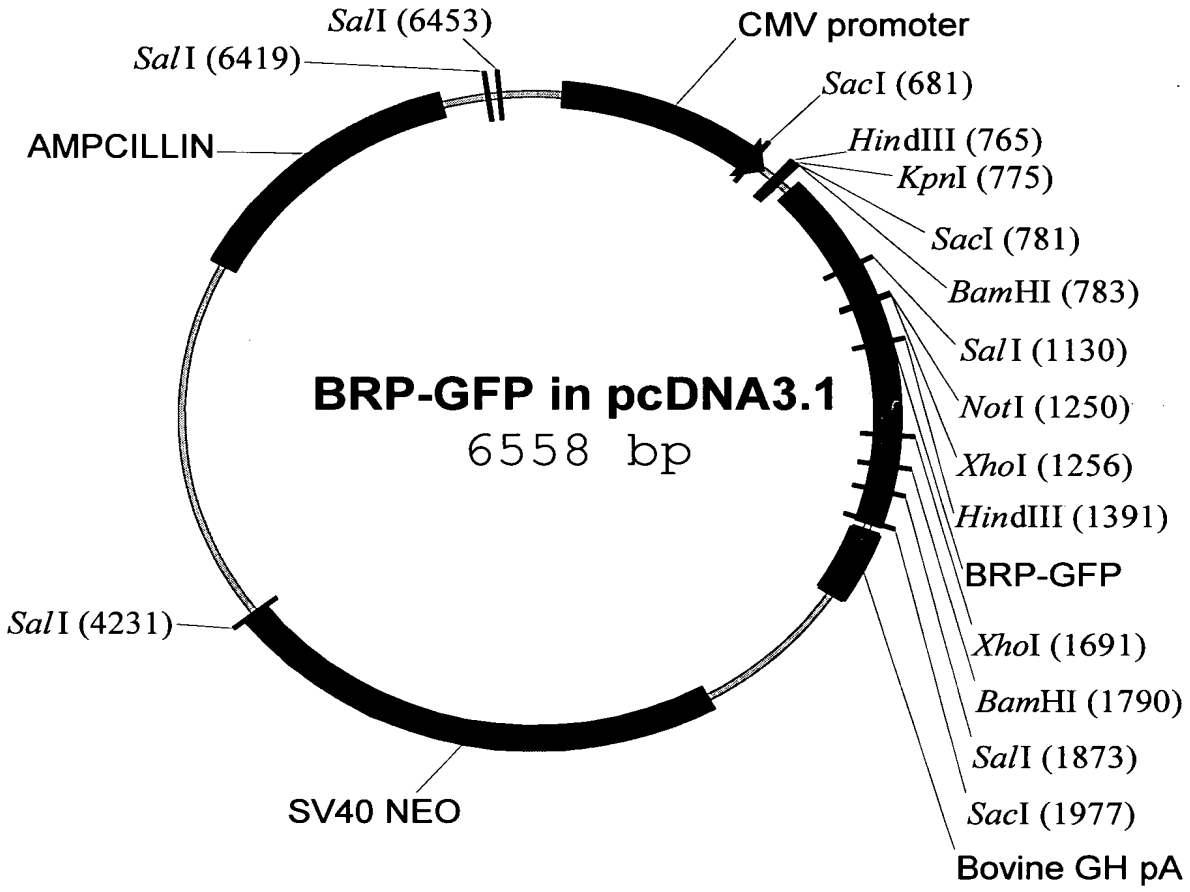

SalI (6453)
CMV promoter
SalI (6419)
SacI (681)
AMPCILLIN
HindIII (765)
KpnI (775)
SacI (781)
BamHI (783)
SalI (1130)
BRP-GFP in pcDNA3.1
6558 bp
NotI (1250)
XhoI (1256)
HindIII (1391)
BRP-GFP
SalI (4231)
XhoI (1691)
BamHI (1790)
SalI (1873)
SV40 NEO
SacI (1977)
Bovine GH pA

Fig. 22

```
                                                                         M  K  L   A  F  L
 771                                                                   GCATGAAGCT GGCATTCCTC

      F  L  G  P   M  A  L   L  L  L   A  G  Y  G   C  V  L   G  A  S   S  G  N  L ·
 841  TTCCTTGGCC CCATGGCCCT CCTCCTTCTG GCTGGCTATG GCTGTGTCCT CGGTGCCTCC AGTGGGAACC
                                                                     PstI
                                                                    ~~~~~~
      .. R  T  F   V  G  C   A  V  R  E   F  T  F   L  A  K   K  P  G  C   R  G  L ·
 911  TGCGCACCTT TGTGGGCTGT GCCGTGAGGG AGTTTACTTT CCTGGCCAAG AAGCCAGGCT GCAGGGGCCT

      . R  I  T   T  D  A  C   W  G  R   C  E  T   W  E  K  P   I  L  E   P  P  Y
 981  TCGGATCACC ACGGATGCCT GCTGGGGTCG CTGTGAGACC TGGGAGAAAC CCATTCTGGA ACCCCCCTAT

      I  E  A  H   H  R  V   C  T  Y   N  E  T  K   Q  V  T   V  K  L   P  N  C  A ·
1051  ATTGAAGCCC ATCATCGAGT CTGTACCTAC AACGAGACCA AACAGGTGAC TGTCAAGCTG CCCAACTGTG
              SalI
             ~~~~~~~
      .. P  G  V   D  P  F   Y  T  Y  P   V  A  I   R  C  D   C  G  A  C   S  T  A ·
1121  CCCCGGGAGT CGACCCCTTC TACACCTATC CCGTGGCCAT CCGCTGTGAC TGCGGAGCCT GCTCCACTGC
                                                                          XhoI
                  BRP    GFP               PstI                      NotI
                 <----   ---->            ~~~~~~~                  ~~~~~~~~
      . T  T  E   C  E  T  I   D  K  G   Q  F  C   R  Y  P  A   Q  W  R   P  L  E
1191  CACCACGGAG TGTGAGACCA TCGATAAAGG GCAATTCTGC AGATATCCAG CACAGTGGCG GCCGCTCGAG

      S  R  M  A   S  K  G   E  E  L   F  T  G  V   V  P  I   L  V  E   L  D  G  D ·
1261  TCTAGAATGG CTAGCAAAGG AGAAGAACTT TTCACTGGAG TTGTCCCAAT TCTTGTTGAA TTAGATGGTG
                                                                     HindIII
                                                                     ~~~~~~
      .. V  N  G   H  K  F   S  V  S  G   E  G  E   G  D  A   T  Y  G  K   L  T  L ·
1331  ATGTTAATGG GCACAAATTT TCTGTCAGTG GAGAGGGTGA AGGTGATGCT ACATACGGAA AGCTTACCCT

      . K  F  I   C  T  T  G   K  L  P   V  P  W   P  T  L  V   T  T  F   S  Y  G
1401  TAAATTTATT TGCACTACTG GAAAACTACC TGTTCCATGG CCAACACTTG TCACTACTTT CTCTTATGGT

      V  Q  C  F   S  R  Y   P  D  H   M  K  R  H   D  F  F   K  S  A   M  P  E  G ·
1471  GTTCAATGCT TTTCCCGTTA TCCGGATCAT ATGAAACGGC ATGACTTTTT CAAGAGTGCC ATGCCCGAAG

      .. Y  V  Q   E  R  T   I  S  F  K   D  D  G   N  Y  K   T  R  A  E   V  K  F ·
1541  GTTATGTACA GGAACGCACT ATATCTTTCA AAGATGACGG GAACTACAAG ACGCGTGCTG AAGTCAAGTT

      . E  G  D   T  L  V  N   R  I  E   L  K  G   I  D  F  K   E  D  G   N  I  L
1611  TGAAGGTGAT ACCCTTGTTA ATCGTATCGA GTTAAAAGGT ATTGATTTTA AAGAAGATGG AAACATTCTC
               XhoI
              ~~~~~~~
      G  H  K  L   E  Y  N   Y  N  S   H  N  V  Y   I  T  A   D  K  Q   K  N  G  I ·
1681  GGACACAAAC TCGAGTACAA CTATAACTCA CACAATGTAT ACATCACGGC AGACAAACAA AAGAATGGAA
                                                BamHI
                                                ~~~~~~
      .. K  A  N   F  K  I   R  H  N  I   E  D  G   S  V  Q   L  A  D  H   Y  Q  Q ·
1751  TCAAAGCTAA CTTCAAAATT CGCCACAACA TTGAAGATGG ATCCGTTCAA CTAGCAGACC ATTATCAACA
                                                                SalI
                                                               ~~~~~~~
      . N  T  P   I  G  D  G   P  V  L   L  P  D   N  H  Y  L   S  T  Q   S  A  L
1821  AAATACTCCA ATTGGCGATG GCCCTGTCCT TTTACCAGAC AACCATTACC TGTCGACACA ATCTGCCCTT

      S  K  D  P   N  E  K   R  D  H   M  V  L  L   E  F  V   T  A  A   G  I  T  H ·
1891  TCGAAAGATC CCAACGAAAA GCGTGACCAC ATGGTCCTTC TTGAGTTTGT AACTGCTGCT GGGATTACAC
                SacI
               ~~~~~~
      .. G  M  D   E  L  Y   K  * · (SEQ ID NO:87)
1961  ATGGCATGGA TGAGCTCTAC AAATAATGAA TTAAACCCGC TGATCAGCCT CGACTGTGCC TTCTAGTTGC
(SEQ ID NO:88)
```

Fig. 23

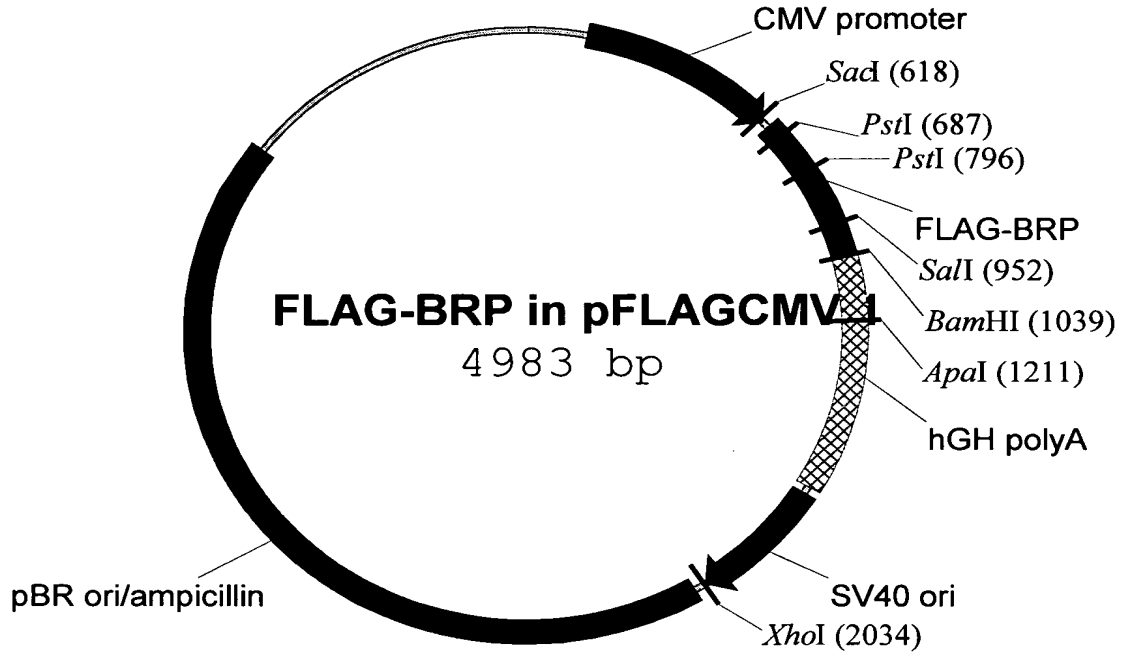


Fig. 24A

```
                                                                SacI
                                                                ~~~~~~~
561   CCGTTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTCGT TTAGTGAACC
                                                                PstI
                          Mouse preprotrypsin leader            ~~~~~~~   FLAG
                                                                          ------>
                        M  S  A  L  L  I  L  A  L  V  G  A  A  V  A  D  Y  K  .
631   GTCAGAATTA ATTCACCATG TCTGCACTTC TGATCCTAGC TCTTGTTGGA GCTGCAGTTG CTGACTACAA

                        BRP
                        ---->
      .  D  D  D  D  K  A  S  S  G  N  L  R  T  F  V  G  C  A  V  R  E  F  T
701   AGACGATGAC GACAAGGCCT CCAGTGGGAA CCTGCGCACC TTTGTGGGCT GTGCCGTGAG GGAGTTTACT
                           PstI
                           ~~~~~~
      F  L  A  K  K  P  G  C  R  G  L  R  I  T  T  D  A  C  W  G  R  C  E  T  .
771   TTCCTGGCCA AGAAGCCAGG CTGCAGGGGC CTTCGGATCA CCACGGATGC CTGCTGGGGT CGCTGTGAGA

      .. W  E  K  P  I  L  E  P  P  Y  I  E  A  H  H  R  V  C  T  Y  N  E  T  .
841   CCTGGGAGAA ACCCATTCTG GAACCCCCCT ATATTGAAGC CCATCATCGA GTCTGTACCT ACAACGAGAC
                                                  SalI
                                                  ~~~~~~~
      .  K  Q  V  T  V  K  L  P  N  C  A  P  G  V  D  P  F  Y  T  Y  P  V  A
911   CAAACAGGTG ACTGTCAAGC TGCCCAACTG TGCCCCGGGA GTCGACCCCT TCTACACCTA TCCCGTGGCC
                                                                BamHI
                                                                ~~~~~~
      I  R  C  D  C  G  A  C  S  T  A  T  T  E  C  E  T  I  *  (SEQ ID NO: 89)
981   ATCCGCTGTG ACTGCGGAGC CTGCTCCACT GCCACCACGG AGTGTGAGAC CATCTGAGGA TCCCGGGTGG
(SEQ ID NO:90)
```

Fig. 24B

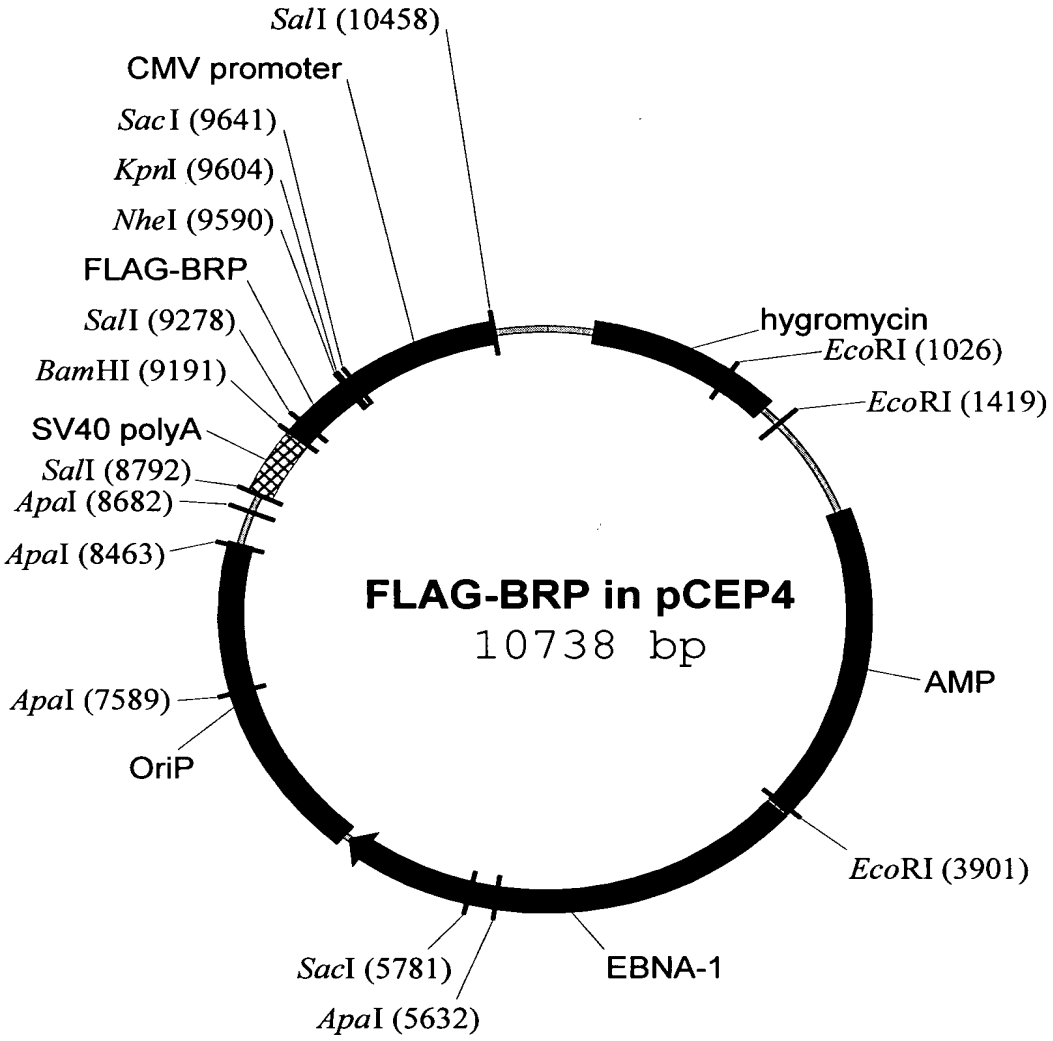

SalI (10458)
CMV promoter
SacI (9641)
KpnI (9604)
NheI (9590)
FLAG-BRP
SalI (9278)
BamHI (9191)
SV40 polyA
SalI (8792)
ApaI (8682)
ApaI (8463)
ApaI (7589)
OriP
SacI (5781)
ApaI (5632)
EBNA-1
EcoRI (3901)
AMP
hygromycin
EcoRI (1026)
EcoRI (1419)
FLAG-BRP in pCEP4
10738 bp

Fig. 25

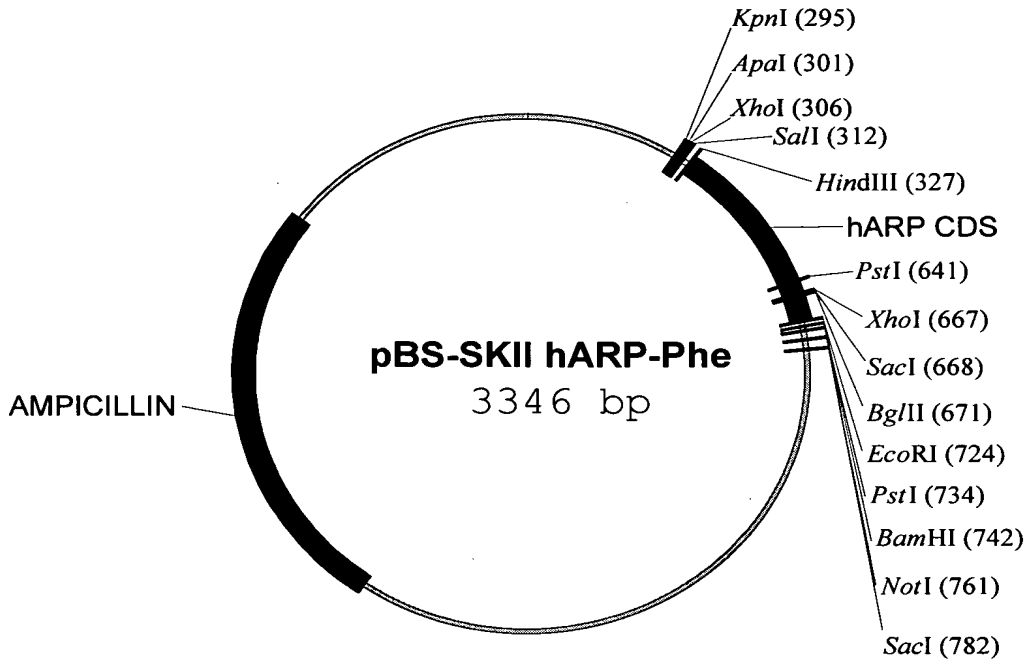


Fig. 26A

```
                 KpnI            XhoI
                 ~~~~~~~         ~~~~~~~
                        ApaI             SalI          HindIII
                        ~~~~~~~          ~~~~~~        ~~~~~~~
                                                                M  P  M  A  S
  281   GGCGAATTGG GTACCGGGCC CCCCCTCGAG GTCGACGGTA TCGATAAGCT TAGTGATGCC TATGGCGTCC

         P  Q  T  L  V  L  Y  L  L  V  L  A  V  T  E  A  W  G  Q  E  A  V  I  P ·
  351   CCTCAAACCC TGGTCCTCTA TCTGCTGGTC CTGGCAGTCA CTGAAGCCTG GGGCCAGGAG GCAGTCATCC

        .. G  C  H  L  H  P  F  N  V  T  V  R  S  D  R  Q  G  T  C  Q  G  S  H ·
  421   CAGGCTGCCA CTTGCACCCC TTCAATGTGA CAGTGCGAAG TGACCGCCAA GGCACCTGCC AGGGCTCCCA

        . V  A  Q  A  C  V  G  H  C  E  S  S  A  F  P  S  R  Y  S  V  L  V  A
  491   CGTGGCACAG GCCTGTGTGG GCCACTGTGA GTCCAGCGCC TTCCCTTCTC GGTACTCTGT GCTGGTGGCC

         S  G  Y  R  H  N  I  T  S  V  S  Q  C  C  T  I  S  G  L  K  K  V  K  V ·
  561   AGTGGTTACC GACACAACAT CACCTCCGTC TCTCAGTGCT GCACCATCAG TGGCCTGAAG AAGGTCAAAG
                                                 XhoI
                                                 ~~~~~~~
              PstI                          SacI  BglII
              ~~~~~~~                       ~~~~~~~~~~~~~
        .. Q  L  Q  C  V  G  S  R  R  E  E  L  E  I  F  T  A  R  A  C  Q  C  D ·
  631   TACAGCTGCA GTGTGTGGGG AGCCGGAGGG AGGAGCTCGA GATCTTCACG GCCAGGGCCT GCCAGTGTGA
                                       PstI
                                       ~~~~~~
                                EcoRI                BamHI                NotI
                                ~~~~~~~              ~~~~~~~              ~~~~~~~
        . M  C  R  L  S  R  Y(SEQ ID NO:91)
  701   CATGTGTCGC CTCTCTCGCT ACGAATTCCT GCAGCCCGGG GGATCCACTA GTTCTAGAGC GGCCGCCACC
(SEQ ID NO:92)
```

Fig. 26B

```
    M  P  M  A  S  P  Q  T  L  V  L  Y  L  L  V  L  A  V  T  E
1   ATGCCTATGGCGTCCCCTCAAACCCTGGTCCTCTATCTGCTGGTCCTGGCAGTCACTGAA   60

    A  W  G  Q  E  A  V  I  P  G  C  H  L  H  P  F  N  V  T  V
61  GCCTGGGGCCAGGAGGCAGTCATCCCAGGCTGCCACTTGCACCCCTTCAATGTGACAGTG  120

    R  S  D  R  Q  G  T  C  Q  G  S  H  V  A  Q  A  C  V  G  H
121 CGAAGTGACCGCCAAGGCACCTGCCAGGGCTCCCACGTGGCACAGGCCTGTGTGGGCCAC  180

    C  E  S  S  A  F  P  S  R  Y  S  V  L  V  A  S  G  Y  R  H
181 TGTGAGTCCAGCGCCTTCCCTTCTCGGTACTCTGTGCTGGTGGCCAGTGGTTACCGACAC  240

    N  I  T  S  V  S  Q  C  C  T  I  S  G  L  K  K  V  K  V  Q
241 AACATCACCTCCGTCTCTCAGTGCTGCACCATCAGTGGCCTGAAGAAGGTCAAAGTACAG  300

                                                F
    L  Q  C  V  G  S  R  R  E  E  L  E  I  L  T  A  R  A  C  Q
301 CTGCAGTGTGTGGGGAGCCGGAGGGAGGAGCTCGAGATCTTAACGGCCAGGGCCTGCCAG  360
                                                C

    C  D  M  C  R  L  S  R  Y  *(SEQ ID NO: 93)
361 TGTGACATGTGTCGCCTCTCTCGCTACTAG  390 (SEQ ID NO:94)
```

Fig. 27

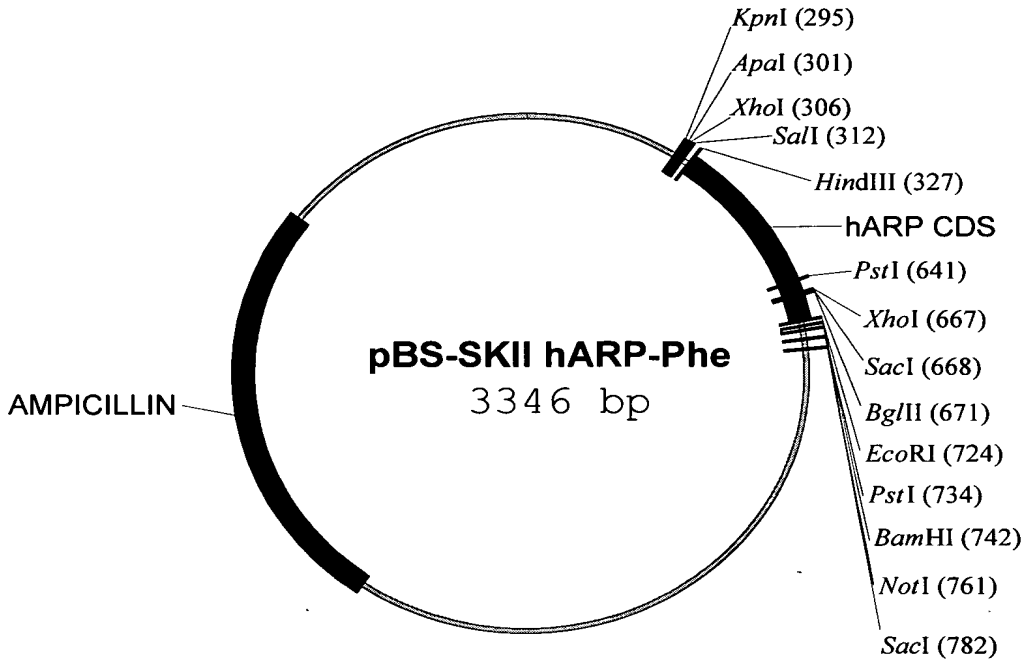


Fig. 28A

```
            KpnI            XhoI
          ~~~~~~~         ~~~~~~~
                 ApaI             SalI          HindIII
               ~~~~~~~          ~~~~~~         ~~~~~~~
                                                      M  P  M  A  S
281  GGCGAATTGG GTACCGGGCC CCCCCTCGAG GTCGACGGTA TCGATAAGCT TAGTGATGCC TATGGCGTCC

      P  Q  T  L  V  L  Y  L  L  V  L  A  V  T  E  A  W  G  Q  E  A  V  I  P  .
351  CCTCAAACCC TGGTCCTCTA TCTGCTGGTC CTGGCAGTCA CTGAAGCCTG GGGCCAGGAG GCAGTCATCC

     ..G  C  H  L  H  P  F  N  V  T  V  R  S  D  R  Q  G  T  C  Q  G  S  H  .
421  CAGGCTGCCA CTTGCACCCC TTCAATGTGA CAGTGCGAAG TGACCGCCAA GGCACCTGCC AGGGCTCCCA

     .V  A  Q  A  C  V  G  H  C  E  S  S  A  F  P  S  R  Y  S  V  L  V  A
491  CGTGGCACAG GCCTGTGTGG GCCACTGTGA GTCCAGCGCC TTCCCTTCTC GGTACTCTGT GCTGGTGGCC

      S  G  Y  R  H  N  I  T  S  V  S  Q  C  C  T  I  S  G  L  K  K  V  K  V  .
561  AGTGGTTACC GACACAACAT CACCTCCGTC TCTCAGTGCT GCACCATCAG TGGCCTGAAG AAGGTCAAAG
                                          XhoI
                                        ~~~~~~~
          PstI                        SacI  BglII
        ~~~~~~~                     ~~~~~~~~~~~~~
     ..Q  L  Q  C  V  G  S  R  R  E  E  L  E  I  F  T  A  R  A  C  Q  C  D  .
631  TACAGCTGCA GTGTGTGGGG AGCCGGAGGG AGGAGCTCGA GATCTTCACG GCCAGGGCCT GCCAGTGTGA
                                   PstI
                                 ~~~~~~
                            EcoRI              BamHI              NotI
                          ~~~~~~~            ~~~~~~~            ~~~~~~~
     .M  C  R  L  S  R  Y(SEQ ID NO:95)
701  CATGTGTCGC CTCTCTCGCT ACGAATTCCT GCAGCCCGGG GGATCCACTA GTTCTAGAGC GGCCGCCACC(SEQ ID NO:96)
```

Fig. 28B

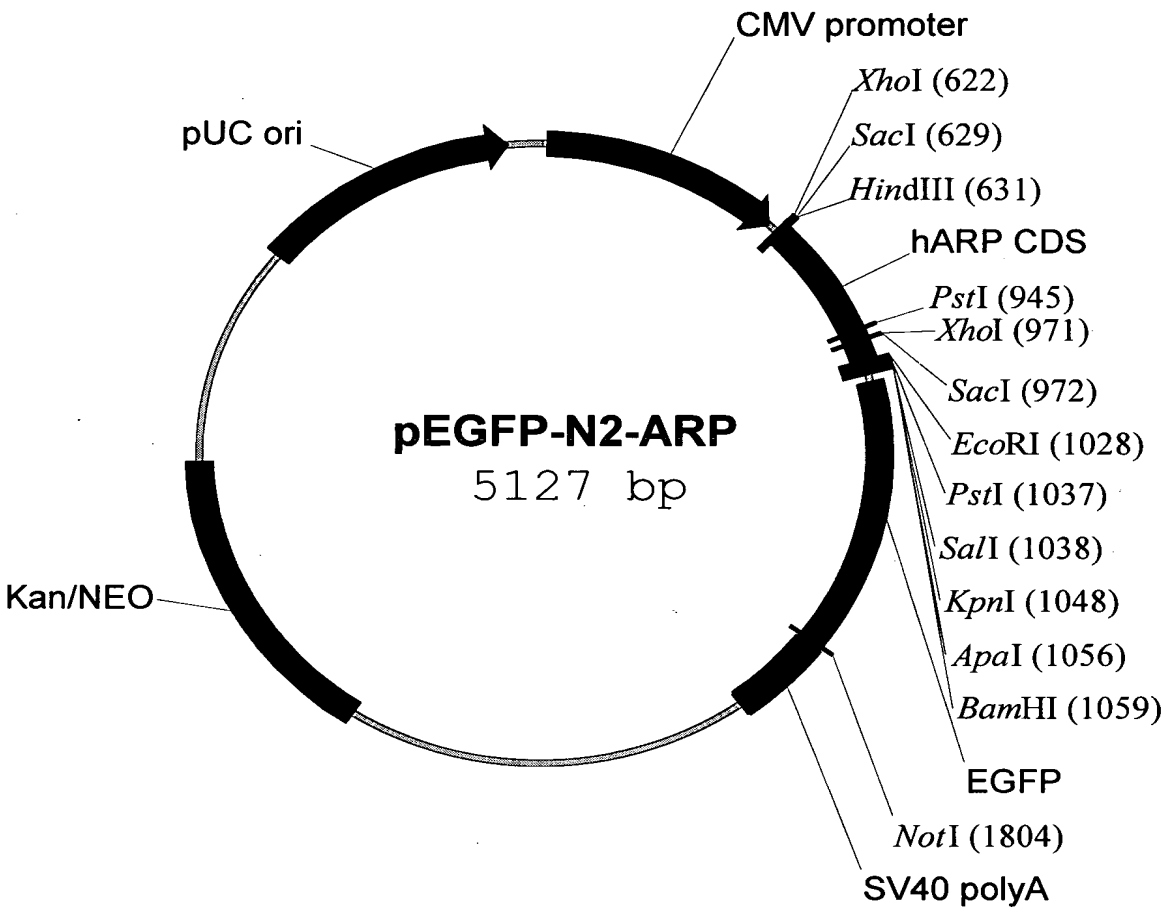

CMV promoter
XhoI (622)
SacI (629)
HindIII (631)
hARP CDS
PstI (945)
XhoI (971)
SacI (972)
EcoRI (1028)
PstI (1037)
SalI (1038)
KpnI (1048)
ApaI (1056)
BamHI (1059)
EGFP
NotI (1804)
SV40 polyA
pUC ori
Kan/NEO
pEGFP-N2-ARP
5127 bp

Fig. 29

```
                M  P  M  A  S  P  Q  T  L  V  L  Y  L  L  V  L  A  V  T  E  A ·
631   AGCTTAGTGA TGCCTATGGC GTCCCCTCAA ACCCTGGTCC TCTATCTGCT GGTCCTGGCA GTCACTGAAG

      ..W  G  Q  E  A  V  I  P  G  C  H  L  H  P  F  N  V  T  V  R  S  D  R ·
701   CCTGGGGCCA GGAGGCAGTC ATCCCAGGCT GCCACTTGCA CCCCTTCAAT GTGACAGTGC GAAGTGACCG

      .Q  G  T  C  Q  G  S  H  V  A  Q  A  C  V  G  H  C  E  S  S  A  F  P
771   CCAAGGCACC TGCCAGGGCT CCCACGTGGC ACAGGCCTGT GTGGGCCACT GTGAGTCCAG CGCCTTCCCT

       S  R  Y  S  V  L  V  A  S  G  Y  R  H  N  I  T  S  V  S  Q  C  C  T  I ·
841   TCTCGGTACT CTGTGCTGGT GGCCAGTGGT TACCGACACA ACATCACCTC CGTCTCTCAG TGCTGCACCA
                                                                  XhoI
                                                                  ~~~~~~
                                        PstI                      SacI
                                        ~~~~~~                    ~~~~~~
      ..S  G  L  K  K  V  K  V  Q  L  Q  C  V  G  S  R  R  E  E  L  E  I  L ·
911   TCAGTGGCCT GAAGAAGGTC AAAGTACAGC TGCAGTGTGT GGGGAGCCGG AGGGAGGAGC TCGAGATCTT
                                                          PstI        KpnI
                                                          ~~~~~~~     ~~
                                              ARP         EcoRI       SalI
                                              <~~~~       ~~~~~~      ~~~~~~
      .T  A  R  A  C  Q  C  D  M  C  R  L  S  R  Y  E  F  C  S  R  R  Y  R
981   AACGGCCAGG GCCTGCCAGT GTGACATGTG TCGCCTCTCT CGCTACGAAT TCTGCAGTCG ACGGTACCGC
       ApaI  BamHI
      ~~~~~~ ~~~~~~~
       G  P  G  I  H  R  P  V  A  T  M  V  S  K  G  E  E  L  F  T  G  V  V  P ·
1051  GGGCCCGGGA TCCACCGGCC GGTCGCCACC ATGGTGAGCA AGGGCGAGGA GCTGTTCACC GGGGTGGTGC

      ..I  L  V  E  L  D  G  D  V  N  G  H  K  F  S  V  S  G  E  G  E  G  D ·
1121  CCATCCTGGT CGAGCTGGAC GGCGACGTAA ACGGCCACAA GTTCAGCGTG TCCGGCGAGG GCGAGGGCGA

      .A  T  Y  G  K  L  T  L  K  F  I  C  T  T  G  K  L  P  V  P  W  P  T
1191  TGCCACCTAC GGCAAGCTGA CCCTGAAGTT CATCTGCACC ACCGGCAAGC TGCCCGTGCC CTGGCCCACC

       L  V  T  T  L  T  Y  G  V  Q  C  F  S  R  Y  P  D  H  M  K  Q  H  D  F ·
1261  CTCGTGACCA CCCTGACCTA CGGCGTGCAG TGCTTCAGCC GCTACCCCGA CCACATGAAG CAGCACGACT

      ..F  K  S  A  M  P  E  G  Y  V  Q  E  R  T  I  F  F  K  D  D  G  N  Y ·
1331  TCTTCAAGTC CGCCATGCCC GAAGGCTACG TCCAGGAGCG CACCATCTTC TTCAAGGACG ACGGCAACTA

      .K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  I  D
1401  CAAGACCCGC GCCGAGGTGA AGTTCGAGGG CGACACCCTG GTGAACCGCA TCGAGCTGAA GGGCATCGAC

       F  K  E  D  G  N  I  L  G  H  K  L  E  Y  N  Y  N  S  H  N  V  Y  I  M ·
1471  TTCAAGGAGG ACGGCAACAT CCTGGGGCAC AAGCTGGAGT ACAACTACAA CAGCCACAAC GTCTATATCA

      ..A  D  K  Q  K  N  G  I  K  V  N  F  K  I  R  H  N  I  E  D  G  S  V ·
1541  TGGCCGACAA GCAGAAGAAC GGCATCAAGG TGAACTTCAA GATCCGCCAC AACATCGAGG ACGGCAGCGT

      .Q  L  A  D  H  Y  Q  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N  H
1611  GCAGCTCGCC GACCACTACC AGCAGAACAC CCCCATCGGC GACGGCCCCG TGCTGCTGCC CGACAACCAC

       Y  L  S  T  Q  S  A  L  S  K  D  P  N  E  K  R  D  H  M  V  L  L  E  F ·
1681  TACCTGAGCA CCCAGTCCGC CCTGAGCAAA GACCCCAACG AGAAGCGCGA TCACATGGTC CTGCTGGAGT
                                                                  NotI
                                                                  ~~~~~~~~~~
      ..V  T  A  A  G  I  T  L  G  M  D  E  L  Y  K  *(SEQ ID NO: 97)
1751  TCGTGACCGC CGCCGGGATC ACTCTCGGCA TGGACGAGCT GTACAAGTAA AGCGGCCGCG ACTCTAGATC
(SEQ ID NO:98)
```

Fig. 30

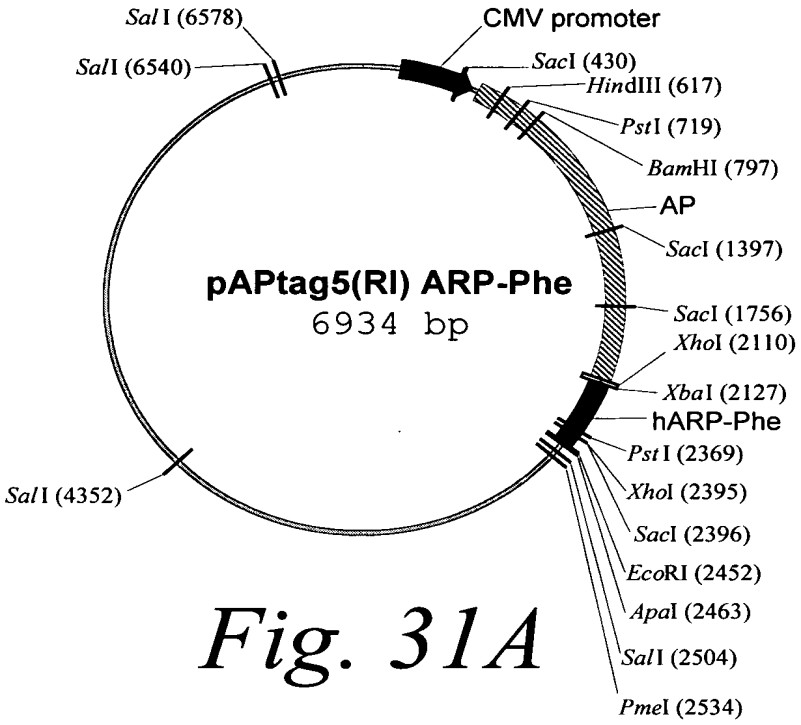


Fig. 31A

```
                                                                    AP
                                                                  <------
      A  A  C  L  E  P  Y  T  A  C  D  L  A  P  P  A  G  T  T  D  A  A  H  P  .
2031  GCCGCCTGCC TGGAGCCCTA CACCGCCTGC GACCTGGCGC CCCCCGCCGG CACCACCGAC GCCGCGCACC
         XhoI
        ~~~~~~~
                                    ARP
                                   ------>
      .. G  Y  L  E  E  A  L  S  L  E  Q  E  A  V  I  P  G  C  H  L  H  P  F  .
2101  CGGGTTATCT CGAGGAAGCG CTCTCTCTAG AACAGGAGGC AGTCATCCCA GGCTGCCACT TGCACCCCTT

      . N  V  T  V  R  S  D  R  Q  G  T  C  Q  G  S  H  V  A  Q  A  C  V  G
2171  CAATGTGACA GTGCGAAGTG ACCGCCAAGG CACCTGCCAG GGCTCCCACG TGGCACAGGC CTGTGTGGGC

       H  C  E  S  S  A  F  P  S  R  Y  S  V  L  V  A  S  G  Y  R  H  N  I  T  .
2241  CACTGTGAGT CCAGCGCCTT CCCTTCTCGG TACTCTGTGC TGGTGGCCAG TGGTTACCGA CACAACATCA
                                                                 PstI
                                                                ~~~~~~~
      .. S  V  S  Q  C  C  T  I  S  G  L  K  K  V  K  V  Q  L  Q  C  V  G  S  .
2311  CCTCCGTCTC TCAGTGCTGC ACCATCAGTG GCCTGAAGAA GGTCAAAGTA CAGCTGCAGT GTGTGGGGAG
                    XhoI
                   ~~~~~~~
                SacI                                                  ARP
               ~~~~~~                                               <------
      . R  R  E  E  L  E  I  F  T  A  R  A  C  Q  C  D  M  C  R  L  S  R  Y
2381  CCGGAGGGAG GAGCTCGAGA TCTTCACGGC CAGGGCCTGC CAGTGTGACA TGTGTCGCCT CTCTCGCTAC
          ApaI
         ~~~~~~~
      EcoRI                    MYC epitope                          SalI          His tag
      ~~~~~~                  ------------>                        ~~~~~~~       ------>
       E  F  G  P  E  Q  K  L  I  S  E  E  D  L  N  S  A  V  D  H  H  H  H  H  H  .
2451  GAATTCGGGC CCGAACAAAA ACTCATCTCA GAAGAGGATC TGAATAGCGC CGTCGACCAT CATCATCATC
            PmeI
           ~~~~~~~~~
      .. H  *          (SEQ ID NO:99)
2521  ATCATTGAGT TTAAACCCGC TGATCAGCCT CGACTGTGCC TTCTAGTTGC CAGCCATCTG TTGTTTGCCC
                                                                  (SEQ ID NO:100)
```

Fig. 31B

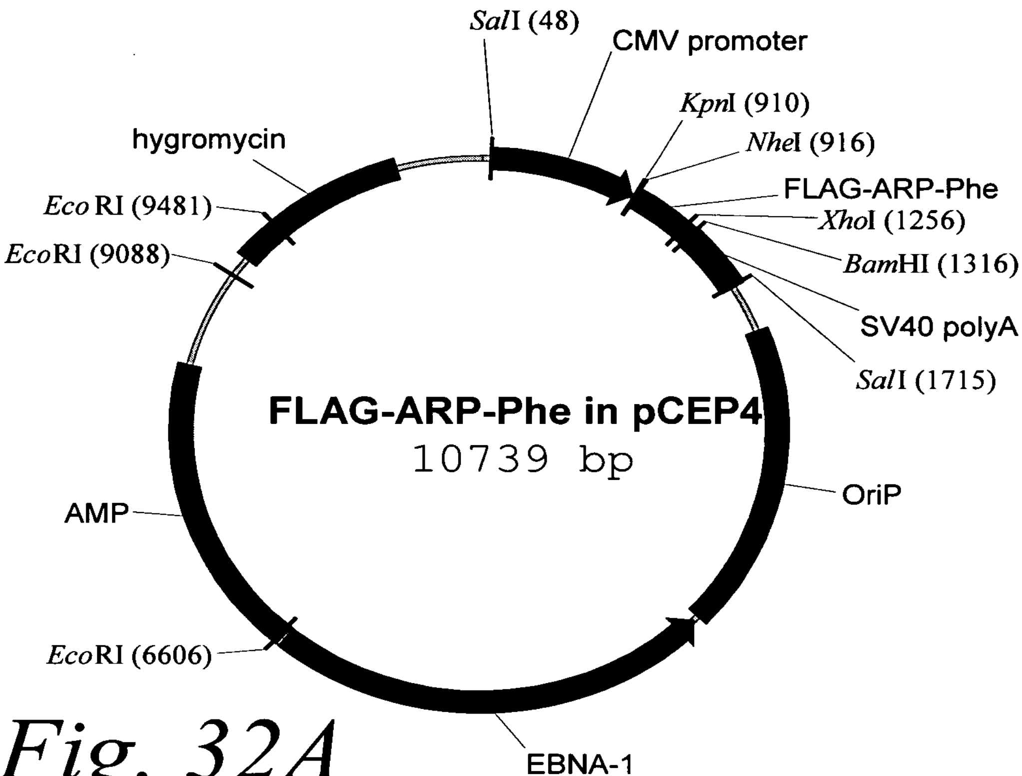


Fig. 32A

```
      NheI       Mouse preprotrypsin leader ------>               FLAG -->
     ~~~~~~~
                     M  S   A  L  L  I   L  A  L   V  G  A   A  V  A  D   Y  K  D·
911  AGCTGCTAGC CACCATGTCT GCACTTCTGA TCCTAGCTCT TGTTGGAGCT GCAGTTGCTG ACTACAAAGA

                   ARP -->
     . D  D  D   K  Q  E  A   V  I  P   G  C  H   L  H  P  F   N  V  T   V  R  S
981  CGATGACGAC AAGCAGGAGG CAGTCATCCC AGGCTGCCAC TTGCACCCCT TCAATGTGAC AGTGCGAAGT

      D  R  Q  G   T  C  Q   G  S  H   V  A  Q  A   C  V  G   H  C  E   S  S  A  F·
1051 GACCGCCAAG GCACCTGCCA GGGCTCCCAC GTGGCACAGG CCTGTGTGGG CCACTGTGAG TCCAGCGCCT

     .. P  S  R   Y  S  V   L  V  A  S   G  Y  R   H  N  I   T  S  V  S   Q  C  C·
1121 TCCCTTCTCG GTACTCTGTG CTGGTGGCCA GTGGTTACCG ACACAACATC ACCTCCGTCT CTCAGTGCTG

                                                                            XhoI
     . T  I  S   G  L  K  K   V  K  V   Q  L  Q   C  V  G  S   R  R  E   E  L  E
1191 CACCATCAGT GGCCTGAAGA AGGTCAAAGT ACAGCTGCAG TGTGTGGGGA GCCGGAGGGA GGAGCTCGAG
                                                                 BamHI
                                                                ~~~~~~~
      I  F  T  A   R  A  C   Q  C  D   M  C  R  L   S  R  Y   *(SEQ ID NO:101)
1261 ATCTTCACGG CCAGGGCCTG CCAGTGTGAC ATGTGTCGCC TCTCTCGCTA CTGAGGATCC AGACATGATA
                                                                       (SEQ ID NO:102)
```

Fig. 32B

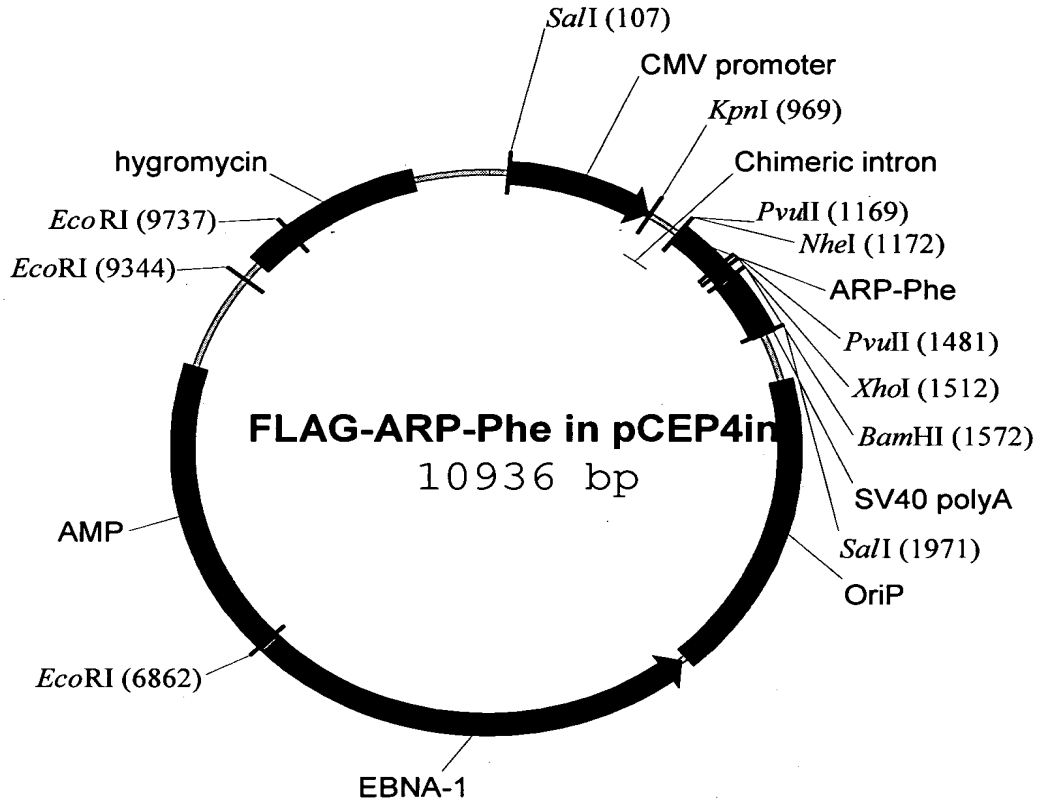
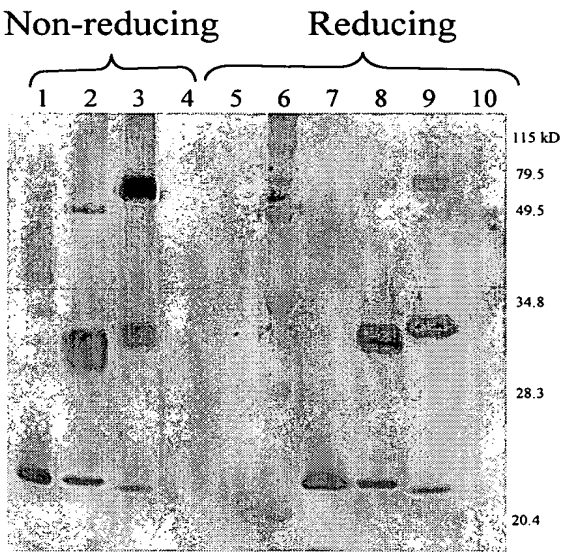

SalI (107)
CMV promoter
KpnI (969)
Chimeric intron
hygromycin
PvuII (1169)
NheI (1172)
EcoRI (9737)
EcoRI (9344)
ARP-Phe
PvuII (1481)
XhoI (1512)
FLAG-ARP-Phe in pCEP4in
10936 bp
BamHI (1572)
SV40 polyA
SalI (1971)
AMP
OriP
EcoRI (6862)
EBNA-1

Fig. 33



Lane	Sample
1.	GFP standard (4ng)
2.	BRP-GFP (5 microliters)
3.	ARP-GFP
4.	control transfection (no DNA)
5.	empty
6.	prestained markers
7.	GFP standard (4ng)
8.	BRP-GFP (5 microliters)
9.	ARP-GFP
10.	control transfection (no DNA)

Note – negative controls and ARP-GFP had same total protein load as for 5 microliter sample of BRP-GFP.

Fig. 34

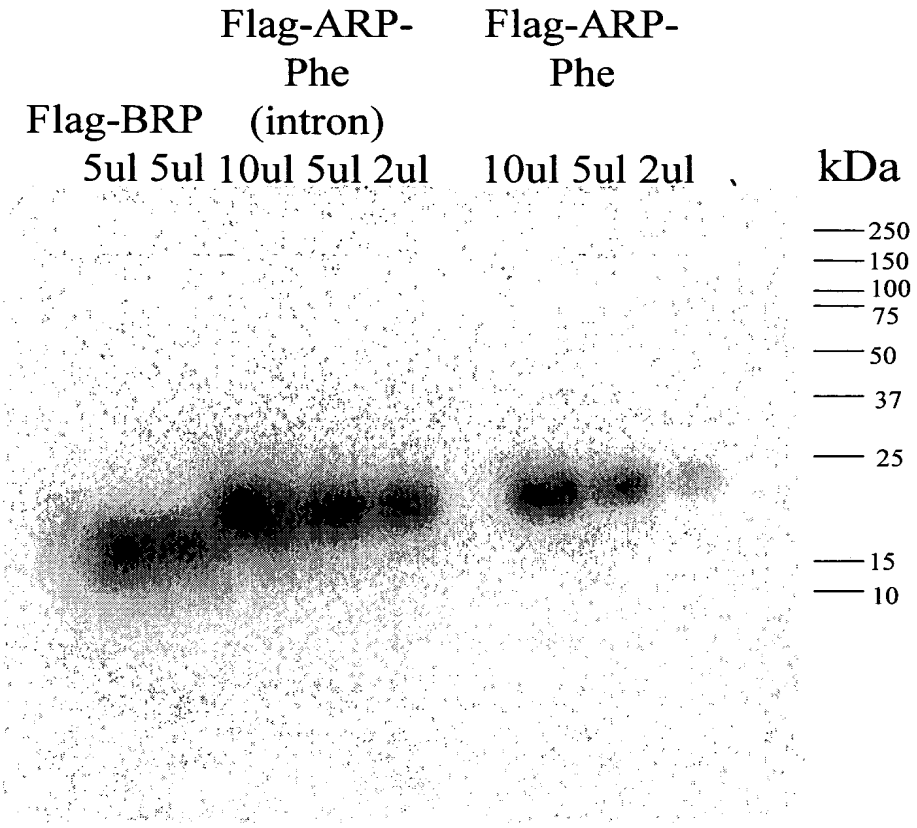
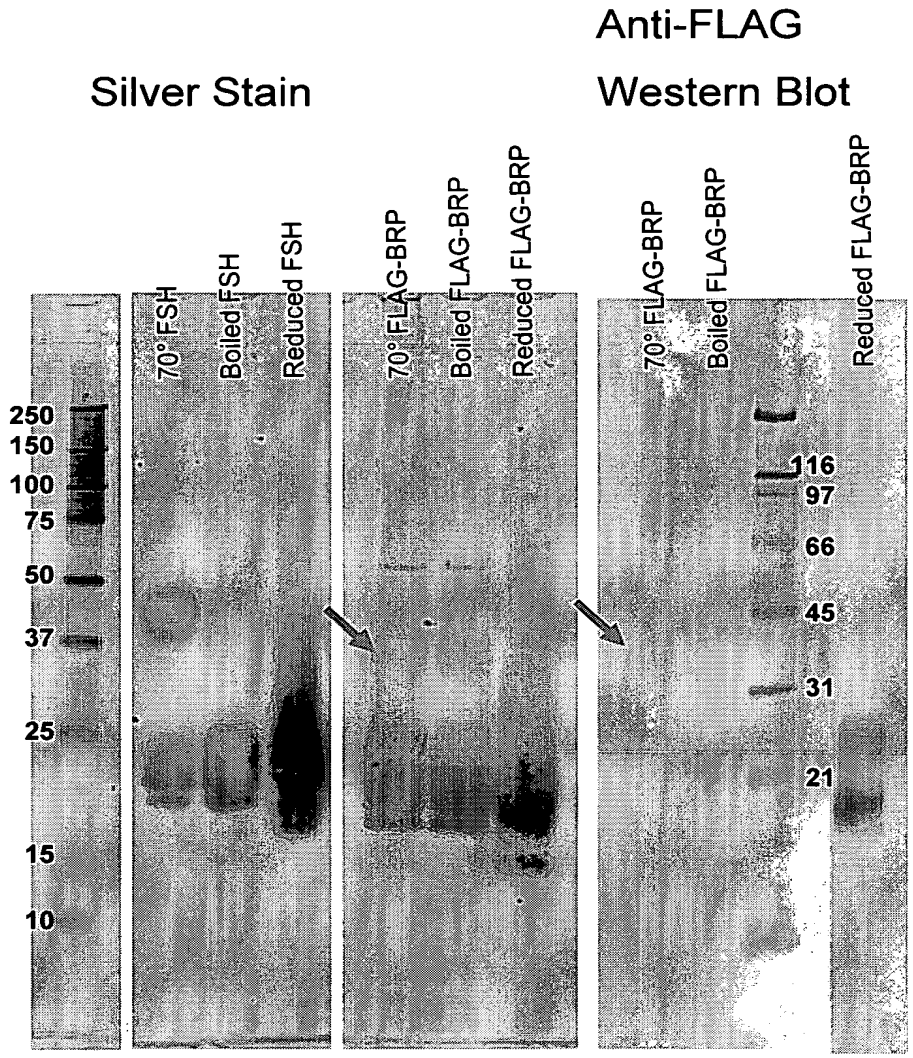

Flag-BRP
5ul 5ul
Flag-ARP-Phe (intron)
10ul 5ul 2ul
Flag-ARP-Phe
10ul 5ul 2ul
kDa
250
150
100
75
50
37
25
15
10

Fig. 35

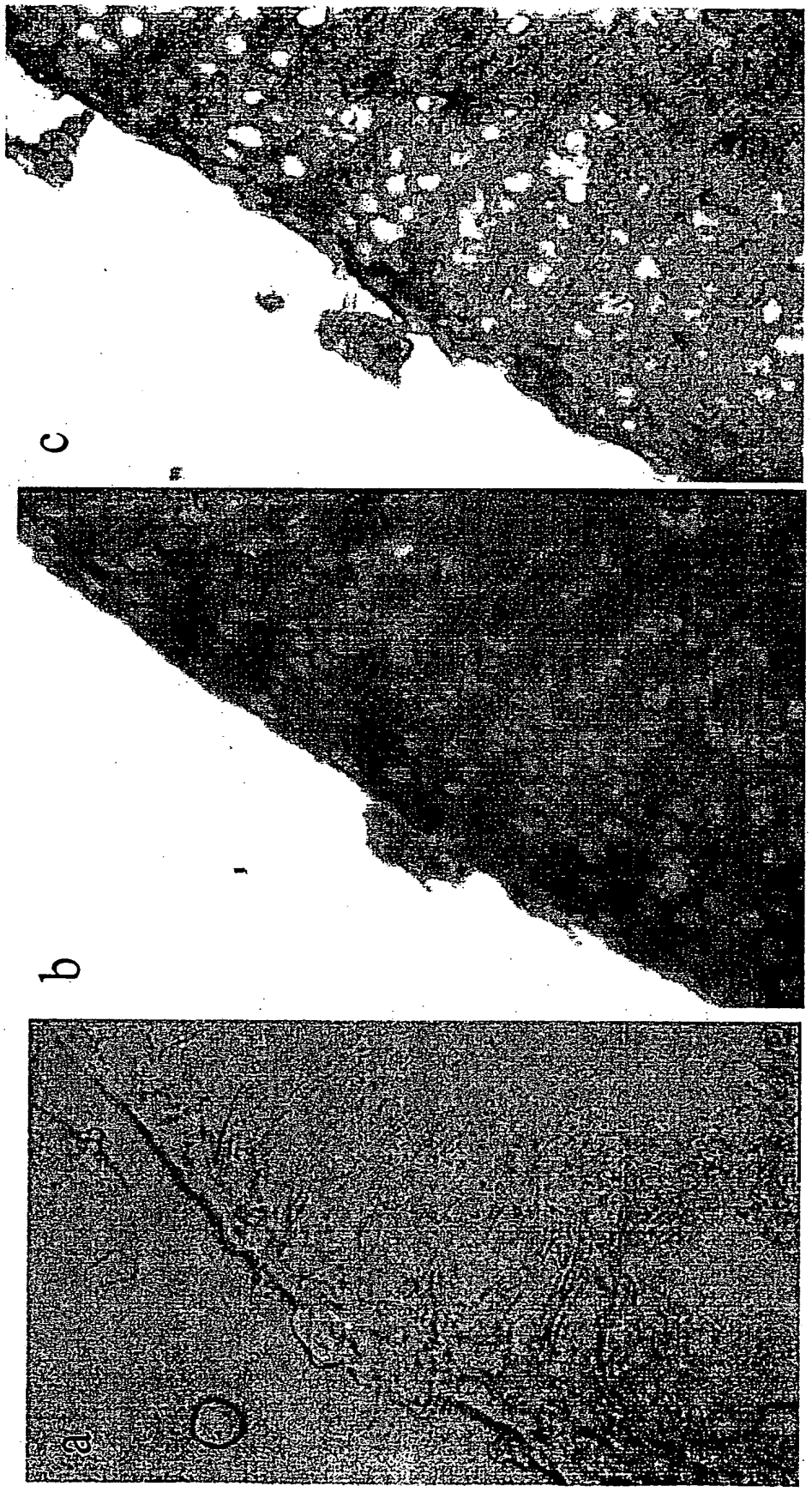


Notes:

- Silver stained (3 left) panels 500 ng loads.
- Western Blots (far right) show 100 ng loads of FLAG-BRP from production lot #2 identified by biotinylated monoclonal anti-FLAG primary antibody and Vector ABC-alkaline phosphatase detection.
- Cyan arrows point to Mr 36 kDa bands which we are interpreting as consistent with disulfide-bonded FLAG-BRP homodimer.

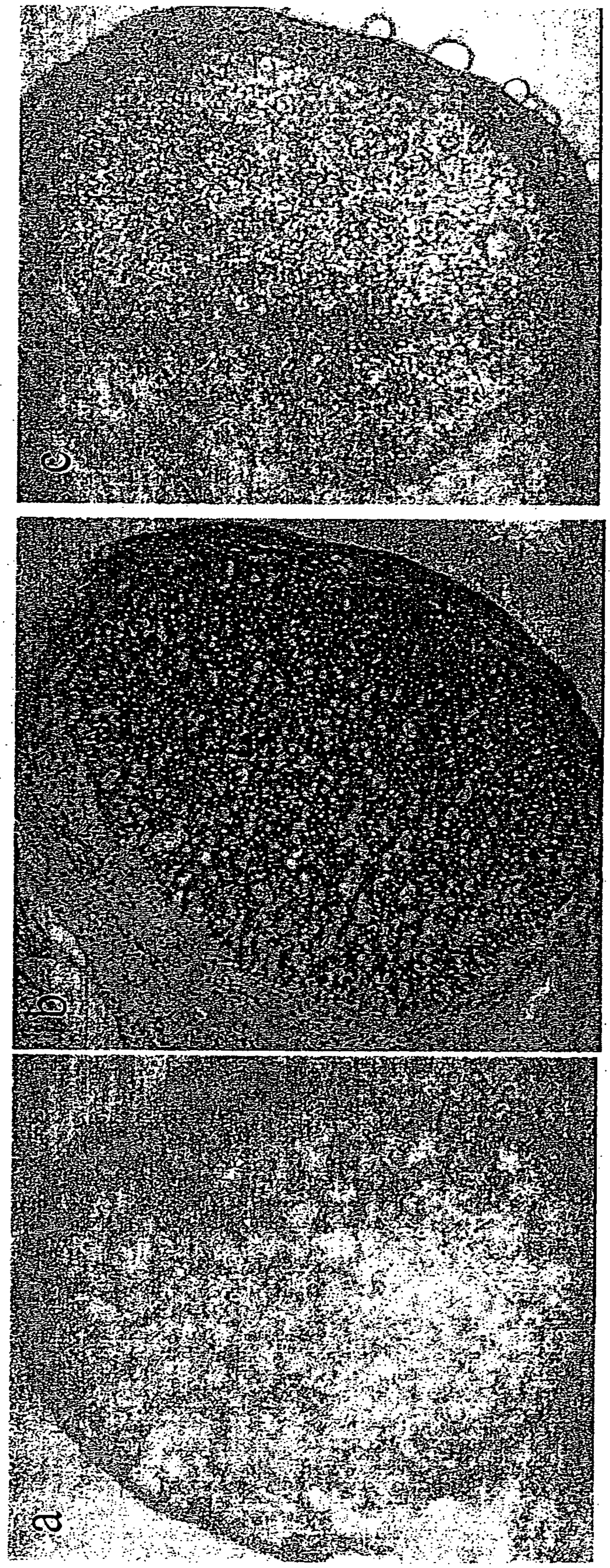
Fig. 36

Fig37. Rat testis



AP AP-BRP AP-BRP + FLAG-BRP

Fig 38. Rat ovary

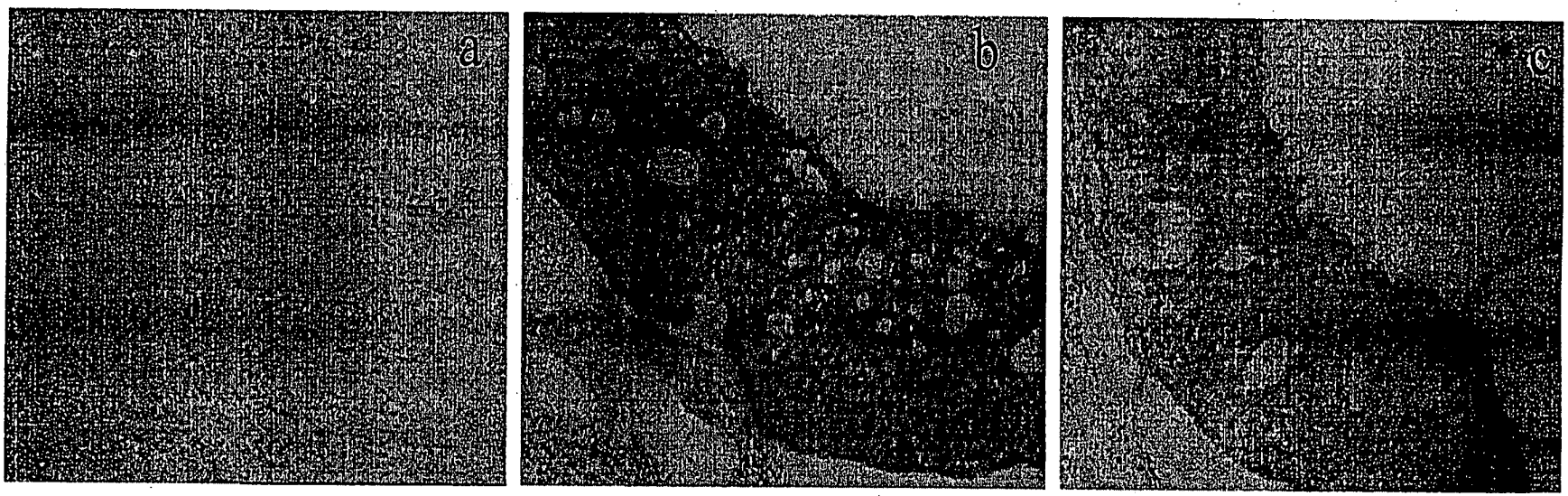


AP

AP-BRP/FLAG-ARP-Phe

AP-BRP/FLAG-ARP-Phe + FLAG-BRP/His-ARP-Phe

Fig 39. Rat ovary

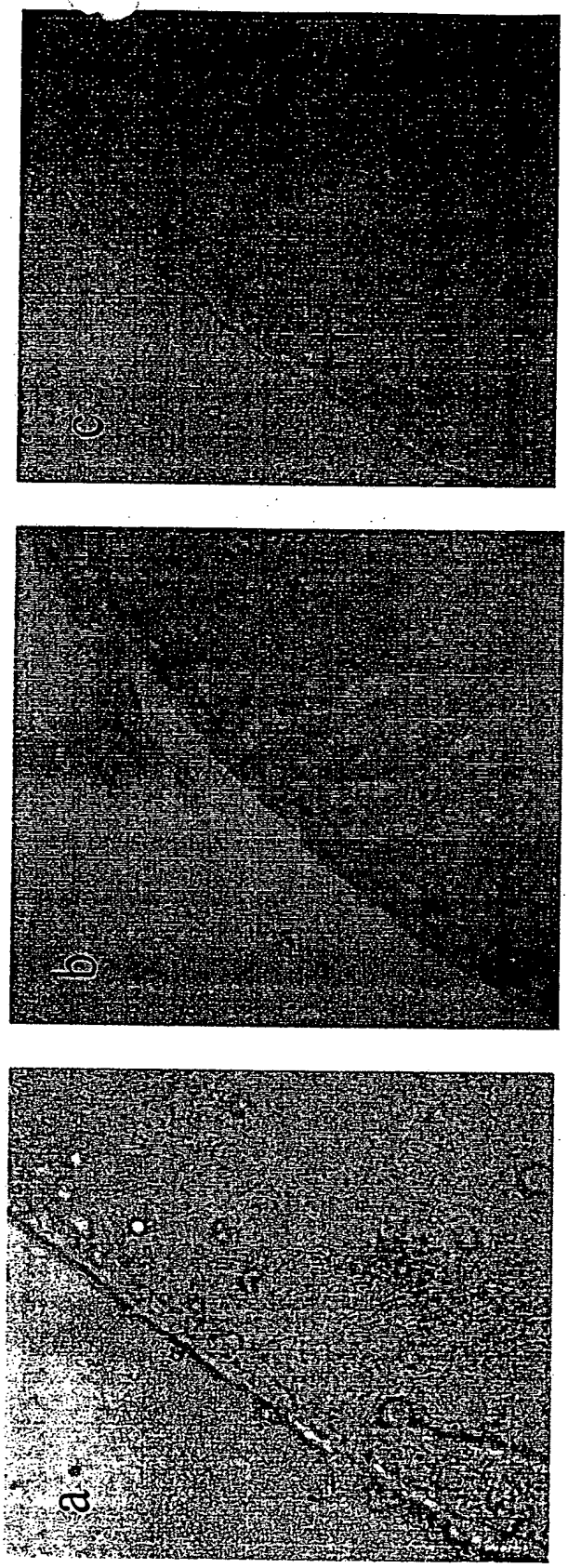


AP

AP-BRP/FLAG-ARP-Phe

AP-BRP/FLAG-ARP-Phe +
FLAG-BRP/His-ARP-Phe

Fig 40. Rat testis



AP

AP-BRP/Flag-ARP-F

AP-BRP/Flag-ARP-F+
FLAG-BRP/His-ARP-Phe

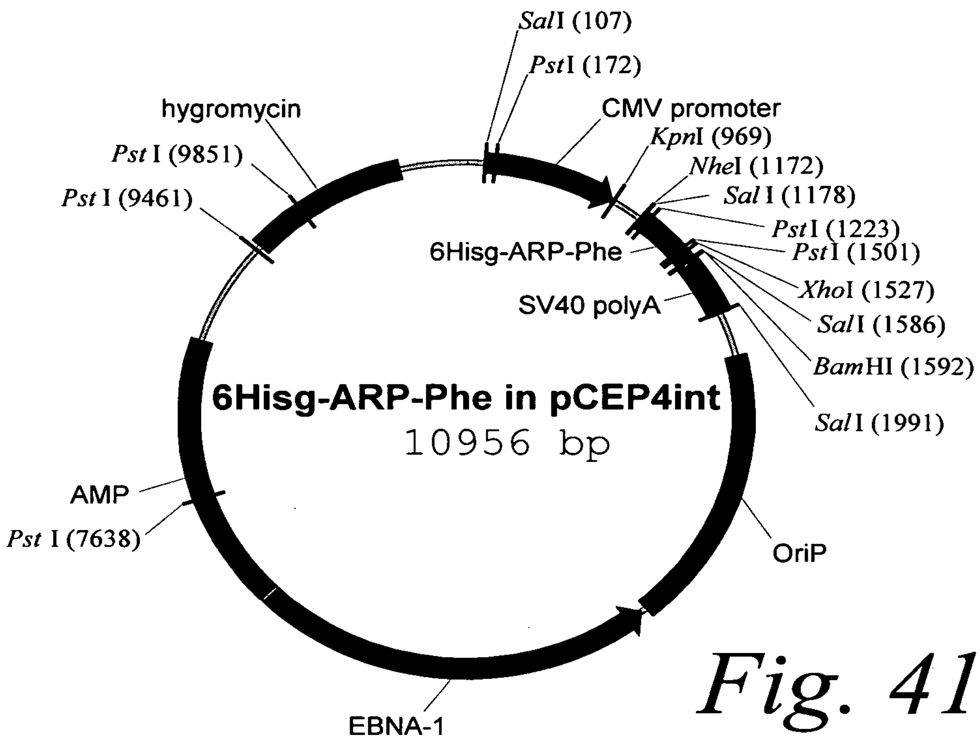


Fig. 41A

```
                                                                    NheI
                                                                  ~~~~~~~~
                                                                         SalI
                                                                        ~~~~~~
                                                                                M  S  A ·
1121   CACTTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGTTCA ATTACCAGCT GCTAGCGTCG ACCATGTCTG
                                    PstI                  6Hisg tag          EK
                                  ~~~~~~~~          ---------------->   ------->
       .. L  L  I   L  A  L   V  G  A  A   V  A  H   H  H  H   H  H  G  D   D  D  D ·
1191   CACTTCTGAT CCTAGCTCTT GTTGGAGCTG CAGTTGCTCA TCATCACCAT CACCATGGTG ACGATGACGA
          ARP
       -------->
       . K  Q  E   A  V  I  P   G  C  H   L  H  P   F  N  V  T   V  R  S   D  R  Q
1261   TAAGCAGGAG GCAGTCATCC CAGGCTGCCA CTTGCACCCC TTCAATGTGA CAGTGCGAAG TGACCGCCAA

        G  T  C  Q   G  S  H   V  A  Q   A  C  V  G   H  C  E   S  S  A   F  P  S  R ·
1331   GGCACCTGCC AGGGCTCCCA CGTGGCACAG GCCTGTGTGG GCCACTGTGA GTCCAGCGCC TTCCCTTCTC

       .. Y  S  V   L  V  A   S  G  Y  R   H  N  I   T  S  V   S  Q  C  C   T  I  S ·
1401   GGTACTCTGT GCTGGTGGCC AGTGGTTACC GACACAACAT CACCTCCGTC TCTCAGTGCT GCACCATCAG
                                   PstI                                  XhoI
                                 ~~~~~~~~                               ~~~~~~
       . G  L  K   K  V  K  V   Q  L  Q   C  V  G   S  R  R  E   E  L  E   I  F  T
1471   TGGCCTGAAG AAGGTCAAAG TACAGCTGCA GTGTGTGGGG AGCCGGAGGG AGGAGCTCGA GATCTTCACG
                                                              BamHI
                                                             ~~~~~~~~
                                                        SalI
                                                      ~~~~~~~~
        A  R  A  C   Q  C  D   M  C  R   L  S  R  Y   *(SEQ ID NO:106)
1541   GCCAGGGCCT GCCAGTGTGA CATGTGTCGC CTCTCTCGCT ACTAGTCGAC GGATCCAGAC ATGATAAGAT
                                                                      (SEQ ID NO:104)
```

Fig. 41B